```
probable phosphoglucomutase - syphilis spirochete

C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004

C;Accession: C71327

R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwn rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McD they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998

A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.

A;Reference number: A71250; MulD:98332770; PMID:9665876

A;Accession: C71327

A;Residues: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-632 <COL>
A;Experimental source: strain Nichols

C;Genetics:
                                                                                                             Ster, E.W.

A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.

A,Reference number: AB2577; MUID:21608589; PMID:11743193

A,Accession: AH2650

A,Status: preliminary

A,Rolecule type: DNA

A,Residues: 1-290 «KIR»

A,Residues: 1-290 «KIR»

A,Residues: 1-290 «KIR»

A,Experimental source: strain C58 (Dupont)

A,Genetics:
A,Genetics: Atu6605

A,Map position: circular chromosome
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; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
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37.1%; Score 46; DB 2; Length 290;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 8; Conservative 3; Mismatches 1; Indels
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Pred. No. 24;
3; Mismatches
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66.7%;
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279 SDLYAGRKSRPA 290
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Best Local Similarity 66.7
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279 SDLYAGRKSRPA 290
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A;Molecule type: DNA
A;Residues: 1-290 <KUR>
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A;Gene: AGR C 1075
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: E7063
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Centles, S.; Hamlin, N.; Holroyd, S.; Randream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Dulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Retus: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Resences: UNIPROT:995206; GB:284725; GB:AL123456; NID:g3261703; PIDN:CAB06589.
A;Experimental source: strain H37RV
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetically: Mycobacterium tuberculosis hypothetical protein Rv0398c
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C;Species: Agrobacterium tumefaciens
C;Date: 11.-Jan-2002 #sequence_revision 11.-Jan-2002 #text_change 09-Jul-2004
C;Accession: AH2650
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
                                                                                                                                                                                                                                                                                               Jacas promoter binding protein-homolog 5 [imported] - garden snapdragon (fragment) C;Species: Antirthinum majus (garden snapdragon) C;Species: Antirthinum majus (garden snapdragon) C;Species: 20-0ct-2000 #sequence_revision 20-0ct-2000 #text_change 09-Jul-2004 C;Accession: T52297 B;Cardon, G.H.; Hoehmann, S.; Klein, J.; Nettesheim, K.; Saedler, H.; Huijser, P. Gene 27, 91-1104, 1999 A;Title: Molecular characterisation of the Arabidopsis SBP-box genes. A;Reference number: Z55236; MUID:99453765; PMID:10524240 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-323 <CAR> A;Molecule type: mRNA A;Residues: 1-323 <CAR> A;Genetics: A;Genetics
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Pred. No. 17;
0; Mismatches 6; Indels
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37.5%; Score 46.5; Di
Best Local Similarity 40.9%; Pred. No. 22;
Matches 9; Conservative 3; Mismatches
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Best Local Similarity 57.1%;
Matches 8; Conservative (
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A,Accession: JC2369
A,Molecule type: mRNA
A,Residues: 1-204 <CHA>
A,Cross-references: UNIPROT:P61314; EMBL:X78167; NID:g515864; PIDN:CAA55026.1; PID:g515
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A/Residues: 2-26;137-173 < CH2>
A/Residues: 2-26;137-173 < CH2>
A/Experimental source: liver
A/Bote: the protein is designated as ribosomal protein L15
C/Genetics:
C/Genetic
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Jul-2000 #sequence revision 21-Jul-2000 #text_change 09-Jul-2004
C;Accession: JC2369; PC2233; JC2236; PC2158
R:Chan, Y.L.; Olvera, J.; Wool, I.G.
                                                                                                                                                                                  Richan, Y.L.; Olvera, J.; Wool, I.G.
Blochem. Blophys. Res. Commun. 201, 108-114, 1994
A;Title: The primary structure of rat ribosomal protein
A;Reference number: JC2236; WUID:94256965; PMID:8198562
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; Pred. No. 19;
5; Mismatches
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Best Local Similarity 40.9%;
Matches 9; Conservative
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A,Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A,Reference number: A83650; MUID:20512582; PMID:11058132
A,Reference number: A83650; MUID:20512582; PMID:11058132
A,Reference mumber: A83650; PMID:11058132
A,Reference mumber: A83650; PMID:11058044
A,Reference 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein At2g14410 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Dreb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: H84516
B;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentto, M.I.; Town, C.D.; Fujii, C.Y.;
B;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentto, M.I.; Town, C.D.; Fujii, C.Y.;
B;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentto, M.I.; Town, C.D.; Fujii, C.Y.;
B;Lin, X.; Kaul, S.; Rounsley, S.D.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.A.; Septerson on analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Recession: H84516
A;Accession: H84516
A;Accession: H84516
A;Accession: DNA
A;Accession: H84516
A;Acce
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.Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
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C;Species: Bacillus halodurans
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Pred. No. 59;
2; Mismatches 4; Indels
                                                                                                                                       Length 632
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55;
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Pred. No.
                                                                                                                                             Score 46;
Pred. No.
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541 YRPI---LYRGREQQDAA 555
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                                                                                                                          37.1%;
58.8%;
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60.0%;
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289 EPIADLIRKKRDRPS 303
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Best Local Similarity 55.6%;
Matches 10; Conservative
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Best Local Similarity 60.0°
Matches 9; Conservative
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Best Local Similarity
                        A;Gene: TP0413
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ribosomal protein L15, cytosolic [validated] - rat

RESULT 15 JC2369

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Gaps

1;

55

DB 1; Length 204; 7; Indels

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein November 10, 2004, 13:38:57; Search time 29:3057 Seconds (without alignments) 431.938 Million cell updates/sec Run on:

US-10-092-750-47 124 Title: Perfect score:

1 PWQYKPIADLYRGRESRPSAPR 22 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 segs, 575374646 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_02:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database :

Pred. No. is the number of result's predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description		fremyella			80					synecho	Ω	36 bovir					Q8h8m4 oryza sativ	m		Q8n5e2 homo sapien		Q6zue3 homo sapien		Q8p5d7 xanthomonas	Q96lw4 homo sapien	0	mus m		4 bacte		9
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BB :	7	~	7	N	-	N	~	N	~	7	N	7	~	~	7	7	~	71	7	7	7	N	~	Н	7	~	N	N	N	N	1
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% Query Match		41.9	41.9	41.1	41.1	41.1	41.1	41.1	40.7	40.7	40.7		40.3	40.3	40.3	40.3	40.3	40.3	39.5	39.5			•	•		٠	39.5	6		39.1	39.1
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SEQUENCE FROM N.A. STRAIN=FD33;

P61367 epinephelus Q75312 monopterus Q75312 monopterus Q713318 acipenser g Q61278 acipenser s Q61278 acipenser s Aa559857 acipenser Aa559858 acipenser Aa559859 acipenser Aa559859 acipenser Q801m6 anaplasma o Q19746 caenorhabdi Q77w59 neurospora Q78641 neurospora Cae85584 neurospora	
RL15_EPICO RL15_MONAL RL15_SINKN Q6T279 Q6T279 Q6T279 AAS59859 AAS59859 AAS59859 AAS59859 AAS59859 AAS59859 AAS59859 AAS59859 AAS59859 Q8GIM6 INX3_CAEEL Q7KW59	
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## ALIGNMENTS

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STRAIN=K1.

X MEDLINE=99310339; PubMed=10382966;
A Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
A Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
Jin-no K., Takahashi M., Sakine M., Baba S.-I., Ankai A., Kosugi H.,
A Takaniya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
A Takaniya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
A Makamura Y., Nomura N., Sako Y., Kikuchi H.;
I. Complete genome sequence of an aerobic hyper-thermophilic
renarchaeon, Aeropyum pernix Kl.";
DNA Res. 6:83-101(1999).
R EMBL, ABO00060; BAA79726.1; -.
R PIR; F72665; F72665.
R Complete proteome; Hypothetical protein.
SEQUENCE 187 AA; 20537 MW; BC1779729470E2A9 CRC64;
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Fremyella diplosiphon (Calothrix PCC 7601)
Bacteria; Cyanobacteria; Nostocales; Microchaetaceae; Fremyella.
NCBI_TaxID=1197;
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43.5%; Score 54; DB 2; Length 187;
Best Local Similarity / 57.9%; Pred. No. 5.9;
Matches 11; Conservative 1; Mismatches 7; Indels
                                                                                                                                                  Aeropyrum permix.
Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
Desulfurococcaceae; Aeropyrum.
NCBI_TaxID=56636;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UDN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein APE0749.
OrderedLocusNames=APE0749;
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                                     187
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                                     PRT;
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                                   PRELIMINARY;
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QGH016
QGH016
AC QGH01
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DT 05-JJ
DD 05-JJ
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OS Prem
OS ROW
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RN [1]
RN SEQU
RESULT 1
Q9YE21
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Klein S., Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC044084; AAH44084.1; -.
HSSP; P13590; 11E5.
                                                  FROM N.A.
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[3]
SEQUENCE FROM N
TISSUE=Embryo;
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Necll-pending-prov protein.

Exhapping a Baevis (African clawed frog).

Exhapping: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.;
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Stowe-Evans E.L., Ford J., Kehoe D.M.; "Genomic DNA Microarray Analysis: Identification of New Genes Regulated by Light Color in the Cyanobacterium Fremyella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41.9%; Score 52; DB 2; Length 211;
47.6%; Pred. No. 14;
iive 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                             STRAIN=FD33;
Stowe-Evans E., Ford J., Kehoe D.M.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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TISSUE=Embryo;
MEDLINE=22341132; PubMed=12454917;
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                                                                                                                                                 J. Bacteriol. 186:4338-4349(2004).
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Dev. Dyn. 225:384-391(2002).
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=8355;
                                                                                                                                       diplosiphon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q7ZXX1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
Q7ZXX1
          RRY REPRET OF REPRETATION OF RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PODITION OF SERVICE SE
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Oliver K., Bowman S., Hall N., Quail M., Rajandream M.A., Harris D.,
del Portillo H.A., Lanzer M., Barrell B.G.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AL360354; CAB96715.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=306 / ATCC 13902 / XV 101;
MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
MEDLINE=22022145; PubMed=12024217; BOI=10.1038/417459a;
Gal Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xanthomonas axonopodis (pv. citri).
Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales;
                                                                                                                                                                                                                                                                                                                        4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium vivax.
Bukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=5855,
                                                                                                                                                                                                                                                     41.9%; Score 52; DB 2; Length 394; 60.0%; Pred. No. 27; 1. Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 40.0%; Pred. No. 45;
Matches 8; Conservative 4; Mismatches 8; Indels
                                                                              PEGEN; PF00017; 19; 3.
SMART; SM00294; 4.1m; 1.
SMART; SM00408; 1Ge2; 1.
PROSITE; PS50835; 1G LIKE; 3.
SEQUENCE 394 AA; 42730 MW; F1141D8E6B69254A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        458 AA; 53134 MW; 785060C82705BB16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
Vir28 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Choline dehydrogenase (EC 1.1.99.1) (CHD) (CDH).
Name=betA, OrderedLocusNames=XACQ718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             458 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 556 AA.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003585; Neurexin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                225 OYKPTAKI----ESRPSMPR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  407 FRYTPVGTFFRGRGRRPGIP 426
                                                                                                                                                                                                                                                                                                                                                                           3 OYKPIADLYRGRESRPSAPR 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 WOYKPIADLYRGRESRPSAP 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xanthomonadaceae; Xanthomonas.
                                                                                                                                                                                                                                               Query Match
Best Local Similarity 60.0%
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                            M. 60, GO:0003842; F:1-pytroline-5-carboxylate dehydrogenase act...;

RO; GO:0003842; F:1-pytroline-5-carboxylate dehydrogenase act...;

RO; GO:000457; F:DNA binding; IEA.

RO; GO:0004591; F:proline dehydrogenase activity; IEA.

RO; GO:0004591; F:proline dehydrogenase activity; IEA.

RO; GO:0006547; F:proline dehydrogenase activity; IEA.

RO; GO:0006557; P:proline dehydrogenase activity; IEA.

RO; GO:0006557; P:metadolism; IEA.

RO; GO:0006562; P:proline catabolism; IEA.

RO; GO:0006562; P:proline catabolism; IEA.

RICEPPO; IPR0012850; Bifunct_PutA.

RICEPPO; IPR001280; MD40.

REPPO; IPR001291; Prodh; 1.

REPPO; PROSONOT; Bifunct_PutA; 1.

RESP: PIRSF000197; Bifunct_PutA; 1.

ROSTIE; PROSONOT; Bifunct_PutA; 1.

ROSTIE; PROSONOT; BILLATIMW; E48350B084EA5ASB CRC64;
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Buell R.C., Liu J., Zaborsky J., Tallon L., Baker B.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Buell R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 51; DB 2; Le:
Pred. No. 1.1e+02;
3; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1483 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AC146506; AAT39963.1; -.
INLETPO; IPR000923; BlueCu 1.
INLETPO; IPR00007; Pept_Aspartic.
INLETPO; IPR001564; RVe.
INLETPO; IPR001504; RVe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       526 RPTADRRQGRDSRPQAHR 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 KPIADLYRGRESRPSAPR 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Solanum demissum (Wild potato)
                    EMBL; AF306633; AAL35755.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41.1%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Putative polyprotein.
Name=PGEC989P08.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ronning C.M.;
Submitted (AUG-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Buell R.;
Submitted (JUN-2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [3]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=50514;
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Q6L420;
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ID Q6
                    셤
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A Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

Cicarelli R.M.B., Coutinho L.L., Cursino-Santos U.R., El-Dorry H.,

Paria J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,

Ratsuvama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.P.,

Locali B.C., Medhado M.A., Madelra A.M.B.N., Martinez-Rossi N.M.,

Martins E.C., Medhado J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira W.C., Oliveira V.R.,

Spinola L.A.F., Takita M.A., Tamura R.B., Teixeira B.C., Tezza R.I.D.,

Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

Setubal J.C., Kitajima J.P.;

R. Comparison of the genomes of two Xanthomonas pathogens with differing

Not specificities "..."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED custstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- FUNCTION: Can catalyze the oxidation of choline to betaine aldehyde and betaine aldehyde to glycine betaine (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Bradyrhizobiaceae, Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reduced acceptor.
-!- COFACTOR: FAD (By similarity).
-!- PATHWAY: Betaine biosynthesis from choline, first step.
-!- SIMILARITY: Belongs to the GMC oxidoreductase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAMAP; MF 00750; -; 1.

InterPro; IPR00172; GMC oxred.

InterPro; IPR07367; GMC oxred.

Pfam; PF0732; GMC oxred.

TIGRRAMS; TIGR01810; betA; 1.

PROSITE; PS00624; GMC OXRED.1; 1.

PROSITE; PS00624; GMC OXRED.1; 1.

Complete proteome; FAD; RIBTO2; 1.

OMPLETE DESCRIPTION: CORRED.2; 1.

OMPLETE DESCRIPTION: CORRED.2; 1.

OMPLETE DESCRIPTION: CORRED.2; 1.

OMPLETE DESCRIPTION: CORRED.2; 1.

OMPLETE DESCRIPTION: CORRED.3; 1.

OMPLETE DE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=GX201;
Wu B., Tang X., Bai X., Tang D., Lu A., Tang J., Ma Q.;
Submitted (ESP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity.
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.1%; Score 51; DB 1;
ilarity 62.5%; Pred. No. 55;
Conservative 1; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1017 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE011702; AAM35607.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              439 OPALDAYRGRÉISPSA 454
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 417:459-463 (2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proline dehydrogenase.
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ACT SITE SEQUENCE

Query Match Local

Best Loc Matches

Name=putA;

Q8VW43; Q8VW43

RESULT 6

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Gaps

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Length 163; Indels

DB 2;

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163 AA; 17939 MW; 1630AB5779679861 CRC64;
                                                               40.7%; Score 50.5; I
61.1%; Pred. No. 17;
iive 2; Mismatches
                                                                                                                                 17
                                                                                                                                                              PWLYDPMSALSRGARESR 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Res. 2:153-166(1995).
EMBL; D90900; BAA16781.1; -.
PIR; S74629; S74629.
                                                                                                                               1 PWOYKPIADLYRG-RESR
EMBL; AY453689; AAS13365.1;
NON_TER 1 1
                                                                                 larity 61.1%;
Conservative
                                                                                                                                                                                                                                                                                                                              Sll1686 protein.
OrderedLocusNames=sll1686;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                               PRELIMINARY;
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Best Local Similarity
Matches 8; Conserv
                                                                                  Local Similarity
ses 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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NCBI_TaxID=129727;
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01-FEB-1997
                                  SEQUENCE
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                                                                   Query Match
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Matches
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                                                                                                                                                                                                                                                                                Solanum demissum (Wild potato).
Bukaryota, Virlidiphantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
                      Gaps
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05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative viral core protein P4b (Fragment).
Bovine papular stomatitis virus.
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Parapoxvirus.
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Bluell R.C., Liu J., Zaborsky J., Tallon L., Baker B.;
"Solanum demissum chromosome 5 BAC PGEC989P08 genomic sequence.";
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
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                      4; Indels
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AC146506; AAT39963.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
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Pred. No. 1.6e+02;
      Pred. No. 1.6e+02;
                                                                                                                                                                  PRT; 1483 AA.
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      46.78;
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75 PWKYEPTVVTYKGKE 89
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                                                                        75 PWKYEPTVVTYKGKE 89
                                                       1 PWQYKPIADLYRGRE
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                      Conservative
                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                               Putative polyprotein.
PGEC989P08.7.
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Submitted (AUG-2003)
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     Best Local Similarity
Matches 7; Conserv
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AAT39963;
01-JUN-2004 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polyprotein.
SEQUENCE 1
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05-JUL-2004
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Matches
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                                                                                                                                                       AAT39963
                                                                                                                                                                       DDTTTTDDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTDDTTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDT
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Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
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05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
0F5-UUL-2004 (TrEMBLrel. 27, Last annotation update)
0FF079 virion core protein P46.
Bovine papular stomatitis virus.
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Sequence analysis of the genome of the unicellular cyanobacterium Synechocysis sp. strain PCC6803, II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECURNCE FROM N.A.
MBDLINE=96127529; PubMed=8590279;
Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
Kajiura M., Tabata S.;
Sequence analysis of the genome of the unicellular cyanobacterium
Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
region from map positions 64% to 92% of the genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ä
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                                                                                                                                                                                                                                                    Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
                                                           (TrEMBLrel. 02, Created)
(TrEMBLrel. 02, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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PRT;
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MEDLINE=97061201; PubMed=8905231;
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PWQYRPVS-IQLGRRPKP 146
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Gaps
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 26, Last annotation update)
101-0CT-2000 (TrEMBLrel. 26, Last annotation update)
101-0CT-2000 (TrEMBLrel. 26, Last annotation update)
101-0CT-2000 (TrEMBLrel. 26, Last annotation update)
102-0CT-2000 (TrEMBLrel. 26, Last annotation update)
103-0CT-2000 (TrEMBLrel. 26, Last annotation update)
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Subunsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,
Shen M., Ronning C.M., Fraser C.M., Somerville C.R., Venter J.C.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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STRAIN=PEST;
Anopheles Geneme Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                Length 197;
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SEQUENCE FROM N.A.
Town C.D., Kaul S.;
Submitted S.;
Submitted AC005499; AAC67366.1; -.
                                                                                                                                                                         preliminary data.
EMBL; AAAB01008960; EAA11143.1; -.
SEQUENCE 197 AA; 22589 WW; BB877FB775441505 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Trimblrel. 10, Created)
(Trimblrel. 10, Last sequence update)
(Trimblrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                             Score 50; DB 2;
Pred. No. 25;
2; Mismatches
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Pred. No. 28;
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).
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InterPro, IPR005162, Retrotrans gag.
Pfam, PF03732, Retrotrans_gag. 1.
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Best Local Similarity 61.9%; Pri
Matches 13; Conservative 2;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=At2g38520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1999
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SEQUENCE 2
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Q9ZVH6
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Q9MOT7
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                                                                                                                         Delhon G., Tulman E.R., Afonso C.L., Iu Z.,
de la Concha-Bermejillo A., Lehmkuhl H.D., Piccone M.E., Kutish G.F.,
Rock D.L.,
"Genomes of the Parapoxviruses Orf Virus and Bovine Papular
Stomtatitis Virus.";
J. Virol. 78:168-177(2004).
EMBL; AV386265, AAR98436.1; -.
InterPro; IPR004972; Pox P48.
Pfam; PF03292; Pox P48; I.
SEQUENCE 683 AA; 74507 MW; 0FA9C718677BBE48 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Delhon G., Tulman B.R., Afonso C.L., Lu Z., de la Concha-Bermejillo A., Lehmkuhl H.D., Piccone M.E., Kutish G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Makaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovine papular stomātitis virus.
Viruses, daDNA viruses, no RNA stage, Poxviridae, Chordopoxvirinae,
Parapoxvirus.
NCSI_TaxID=129727;
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J. Virol. 78:168-177(2004).
EMBL; AY386265; AAR98436.1; -
SEQUENCE 683 AA; 74507 MW; 0FA9C718677BBE48 CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              683 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 AA.
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40.7%; Score 50.5; D

Best Local Similarity 61.1%; Pred. No. 82;
Matches 11; Conservative 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-WAR-2004 (TrEMBLrel. 27, Created) 02-WAR-2004 (TrEMBLrel. 27, Last seq 02-WAR-2004 (TrEMBLrel. 27, Last ann ORF079 virion core protein P4b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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Best Local Similarity 61.19
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                                                                                               PubMed=14671098;
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PubMed=14671098;
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AAR98436

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RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL, Ali61507; CAB77930.1; -.
DR PIR, A85076; A85076.
KW Hypothetical protein.
SQ SEQUENCE 282 AA; 31518 MW; 1A691C1C95991A03 CRC64;

QUELY MATCH

QUELY MATCH

GOOD Similarity 60.0%; Pred. No. 37;

BOBET Local Similarity 60.0%; Pred. No. 37;

MATCHES 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
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Search completed: November 10, 2004, 14:50:04 Job time : 31.3057 secs

5 KPIADLYRGRESRPS 19 :|||||:| 188 EPIADLFRKKRERPS 202

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Sequence 2, Application US/08100709
Patent No. 5322697
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Tan, Vuping
APPLICANT: Jany, Christine S.
APPLICANT: Jany, Christine S.
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: PACILLUS THURINGIENSIS CIVETA AND CIVETS
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel
                                                          Sequence 2
Sequence 4
Sequence 6
Sequence 8
Sequence 1
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Sequence 4
Sequence 6
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ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/100,709
FILING DATE: 1993029
CLASSIFICATION: SIP
ATTORNEY AGENT INFORMATION:
NAME: EGOLf. Christopher
REGISTRATION NUMBER: 27633
REFERENCE/POCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 2:
SEQUENCE CHRACTERISTICS:
'PMNTH' 1167 amino acids
US-08-980-071-10
US-08-980-071-12
US-08-980-071-59
US-08-757-536-4
US-08-757-536-6
US-08-757-536-8
US-08-757-536-8
US-08-757-536-8
US-08-757-536-10
US-08-757-536-10
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US-09-314-093-8
US-09-314-093-8
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US-09-314-093-8
US-09-314-093-8
                                                                                                                                                                                                                                                                                     ALIGNMENTS
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Best Local Similarity 61.5
Matches 8; Conservative
                 MOLECULE TYPE: protein US-08-100-709-2
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LLQFLLNNFVPGG
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  TOPOLOGY:
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US-08-100-709-2
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'GGTZ_6/ptodata1/jaa/5A_COMB.pep:*
'GGTZ_6/ptodata1/jaa/6A_COMB.pep:*
'GGTZ_6/ptodata1/jaa/6A_COMB.pep:*
'GGTZ_6/ptodata1/jaa/6B_COMB.pep:*
'GGTZ_6/ptodata1/jaa/6B_COMB.pep:*
'GGTZ_6/ptodata1/jaa/PCTUS_COMB.pep:*
'GGTZ_6/ptodata1/jaa/backfiles1.pep:*
                5.1.6
Compugen Ltd.
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                                                                                                                                                                                                                                                      478139 seqs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
              GenCore version (c) 1993 - 2004
                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                   protein search, using sw model
                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                   US-10-092-750-48
91
1 LFSVLLRYLADNFLPGGS 18
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Maximum DB seq length: 200000000
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Match Length
                            Copyright
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                                                                                                                                                      Title:
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Gaps

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Philadelphia
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                                                                                                                  COUNTRY: U
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                                                                                                                                                                                                       Sequence 2, Application US/08176865

Patent No. 5615319

GENERAL INFORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Tan, Yuping
APPLICANT: Tan, Yuping
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Madel

STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STRATE: Pennsylvania
CUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
COMPUTER: 1BM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,865
FILING DATE: 30-DEC-1993
CLASSIFICATION NUMBER: US/08/176,865
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BG016, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 27633
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LENGTH: 1167 amino acids
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Best Local Similarity 61.5
Matches 8; Conservative
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TOPOLOGY: linear
                                                                                                                                                 RESULT 2
US-08-176-865-2
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Pred. No. 20;
4; Mismatches 1; Indels
                                                                                                                                             Sequence 6, Application US/08448170
Patent No. 5723758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 8, Application US/08961803; Patent No. 6150589; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.7%;
                              41 LLQFLLNNFVPGG 53
        5 LLRYLADNFLPGG 17
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Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-448-170-6
                                                                                                        RESULT 6
US-08-448-170-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
US-08-961-803-8
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Patent No. 59468

Patent No. 594568

Patent No. 59468

Patent No. 59
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                                                        REFERENCE/DOCKET NUMBER: 7205
TELECOWINICATION INFORMATION:
TELEPHONE: 215-75-1590
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENDRY: 1167 amino acids
TYPE: amino acids
ATTORNEY/AGENT INFORMATION:
NAME: Egolf, Christopher
REGISTRATION NUMBER: 27633
                                                                                                                                                                                                                                                                                      52.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1167 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                              41 LLQFLLNNFVPGG 53
                                                                                                                                                                                                                                                                                                                             8; Conservative
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) MOLECULE TYPE: protein
US-08-779-046-2
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Best Local Similarity
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US-08-881-340-2
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GENERAL INFORMATION:

APPLICANT: VON TERSCH, Michael A.

APPLICANT: VON TERSCH, MICHAEL A.

TITLE OF INVENTION: BACILIUS THURINGIENSIS CTYET! TOXIN GENE
TITLE OF INVENTION: AND PROTEIN TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Panich Schwarze Jacobs & Nadel c/o A.S.

ADDRESSEE: Nadel
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pred. No. 20; 1; Indels
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 48; DB 4; Length 1168;
Pred. No. 20;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUDLESSEE: NAGEL
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
CUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/032,364
FLING DATE: 19930317
CLASSIEDATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: EGOLÉ, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 27633
REFERENCE/DOCKET NUMBER: 27633
TELECOMMUNICATION INFORMATION:
TELECOMU
TITLE OF INVENTION: and Methods of Use
FILE REFERENCE: MECO201
; CURRENT APPLICATION NUMBER: US/09/661,322A
; CURRENT FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 22
; ENGTH: 1168
; TYPE: PRT
; CORANISM: Bacillus thuringiensis
US-09-661-322A-22
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US-09-489-039A-12404
; Sequence 12404, Application US/09489039A
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Best Local Similarity 61.5%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1170 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 LLQFLLNNFVPGG 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S LLRYLADNFLPGG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-032-364-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
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Sequence 22, Application US/09661322A

Sequence 22, Application US/0966132A

Sequence 22, Application US/0966132A

Sequence 22, Application US/0966132A

Sequence 22, Application US/0966132A

SEQUENCE INFORMATION:

APPLICANT: Baum, James A.

APPLICANT: Donovan, William P.

APPLICANT: Glimer, Amy J.

APPLICANT: Rupar, Mark J.

APPLICANT: Rupar, Mark J.

TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compos
                                                                         APPLICANT: Cummings, David A.
APPLICANT: Cannon, Raymond J.C.
APPLICANT: Stannon, Raymond J.C.
APPLICANT: Stelman, Steve
APPLICANT: Stelman, Steve
TITLE OF INVENTION: No. 6150589el Bacillus thuringiensis Isolate Denoted
TITLE OF INVENTION: B.t. PSILSGC2, Active Against Lepidopteran Pests, and Genes
TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
NUMBER OF SEQUENCES:
ADDRESSEE: Jay M. Sanders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA

ZIP: 32606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IMP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,803
FILING DATE: 31-CT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/069,902
FILING DATE: 10-JUNE-1993
CLASSIFICATION BOTA:
APPLICATION NUMBER: US 07/759,247
FILING DATE: 13-SEPT-1991
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/448,170
FILING DATE: 13-SEPT-1991
CLASSIFICATION NUMBER: US 08/448,170
FILING DATE: 13-SEPT-1991
CLASSIFICATION NUMBER: US 08/448,170
FILING DATE: 33-MAY-1995
CLASSIFICATION NUMBER: US 08/448,170
FILING DATE: 33-MSY 08/00
ATTORNEY/AGENT INFORMATION:
NAME: SAGGERS, JAY M.
REFIRENCE/OPCKET NUMBER: M/S 102DCD1
TELEPRANT (352) 375-8800
INFORMATION FOR EQ. 100
TELEPRANT (352) 375-8800
INFORMATION FOR EQ. 100
INFORMATION F
                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Jay M. Sanders
STREET: 2421 N.W. 41st Street, Suite A-1
COUNTRY: Galnesville
STATE: Florida
                                      Payne, Jewel
Cummings, David A.
Cannon, Raymond J.C.
Narva, Kenneth E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 LLRYLADNFLPGG 17
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STRANDEDNESS: Bil
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Matches
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    GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUMBER: US/09/489,039A
CURRENT PELLOATION NUMBER: US 60/117,747
PRIOR PELLOATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
ESCO ID NO 12404
LENGTH: 696
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Patent No. 6043415

GENERAL INFORMATION:
APPLICANT: STRIZHOV, Nicolai
APPLICANT: SCHELL, Jeff
APPLICANT: ZILBERTSTEIN, Aviah
APPLICANT: KILLER, Menachem
APPLICANT: KELLER, Menachem
APPLICANT: KONCZ, Csaba
TITLE OF INVENTION: SYNTHETIC BACILLUS THURINGIENSIS GENE
TITLE OF INVENTION: ENCODING AN INSECT TOXIN
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                               Score 46; DB 4; Length 696; Pred. No. 24; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CUMPLAIN: CULT

ZIP: 2007

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/771,986A
FILING DATE: 23-DEC-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
REFERENCE (2020) 672-5300
TELEFONE: (2020) 672-5300
TELEFONE: (202) 672-5300
TELEFONE: (2020) 672-5300
TELEFONE: (2020) 672-5300
TELEFONE: (2020) 672-5300
TELEFONE: (2020) 672-5300
                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237 FPVSLRISADDFLKGGN 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 FSVLLRYLADNFLPGGS 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                               50.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        630 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 58.8<sup>§</sup>
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-771-986A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
US-08-771-986A-2
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Length 630;

Score 45; DB 3; Pred. No. 31;

49.5%;

Query Match Best Local Similarity

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HAPLOTYEE: not applicable
TISSUE TYPE: not applicable
TISSUE TYPE: unicellular organism
INMEDIATE SOURCE: 7.29
INMEDIATE SOURCE: 7.29
ILIBRARY: not applicable
CLONE: not applicable
CLONE: not applicable
CHROMOSOMES/SEGMENT: not applicable
MAP POSITION: not applicable
MAP POSITION: not applicable
MAP POSITION: or applicable
MAP POSITION: 1 is the sequence in claim 6, and
NAME/KEY: SEQ. ID NO: 2 : is the sequence in claim 6, and
NAME/KEY: not available
ILOCATION: not available
ILOCATION: MATHOD: by experiment
THER INFORMATION: specifically toxic to insects of spodoptera
OTHER INFORMATION: genus confers Spodoptera resistance being expressed in trans
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       Gaps
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                                                                                                                                                                                           Sequence 2, Application US/08769802A;
Sequence 2, Application US/08769802A;
Patent No. 611068
GENERAL INFORMATION:
APPLICANT: Strizhov, Nicolai, Koncz, Csaba; Schell, Jeff;
TITLE OF INVENTION: Gene Synthesis Method
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS: 1
ADDRESSEE: Wagman, Cohen, Leitner & Myers, P.C.
STREET: 900 17th Street, N.W., Suite 1000
STATE: D.C.
       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette 3.5 inch, 1.44 Mb storage COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
       2,
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COPERATING SISTEM.

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/769,802A
FILING DATE: 20 - DEC - 1996
CLASSIFICATION: 435
PRICK APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/027,896
FILING DATE: 07 - OCT - 1996
ATTORNEY/AGENT INFORMATION:
NAME: COCHEN, HEREBER: 03.63.004/P
REFERENCE/DOCKET NUMBER: 03.63.004/P
TELEPHONE: (202) 463 - 6915
INFORMATION FOR EAQ ID NO: 2:
ELENGTH: 630 amino acid residues
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: truncated protein
HYPOTHETICAL: no
       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Bacillus thuringiensis
STRAIN: K26-21, MR1-37, subsp. aiz
INDIVIDUAL ISOLATE: not applicable
HAPLOTYPE: not applicable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-terminal fragment
       4;
                                               5 LLRYLADNFLPGG 17
                                                                             41 LVQFLVSNFVPGG 53
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: no
FRAGMENT TYPE: N
ORIGINAL SOURCE:
                                                                                                                                                                RESULT 12
US-08-769-802A-2
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APPLICANT: SANCHIS, Vincent

APPLICANT: SANCHIS, Didier

MENOU, Ghislaine

MENOU, Ghislaine-Marie

LECADET, Marquerite-Marie

MARTOURET, Daniel

DEDONDER, RAYMOND

TITLE OF INVENTION: NUCLEOTIDES ENDOWED WITH A LARVICIDAL ACTIVITY TOWARDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45; DB 1; Length 823;
Pred. No. 42;
4; Mismatches 2; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
             COMPUTER: REALBLE FORDY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SETEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,551
FILING DATE: 05-JUM-1995
CLASSIFICATION NUMBER: US 08/251,652
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/458,754
FILING DATE: 11-DEC-1989
PRIOR APPLICATION NUMBER: EP 88 401 121.4
FILING DATE: 06-MAY-1988
PRIOR APPLICATION NUMBER: FR 87 08090
FILING DATE: 10-JUN-1987
ATTONEY/AGENT INFORMATION:
ATTONEY/AGENT INFORMATION:
ATTONEY/AGENT INFORMATION:
ATTONEY/AGENT INFORMATION:
ATTONEY/AGENT INFORMATION:
ATTONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSE: BURNS, DOANE, SWECKER & MATHIS STRET: P.O. Box 1404
CITA Alexandria
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       010830-073
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Patent No. 6310035
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: HUNTINGTON, R. D.
REGISTRATION NUMBER: 27,903
REFERENCE/DOCKET NUMBER: 010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                823 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 LLRYLADNFLPGG 17
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41 LVQFLVSNFVPGG 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-09-037-621A-2
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Sequence 8203, Application US/09328352
Sequence 8203, Application US/09328352
Sequence 8203, Application of all General Information:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRESENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 8203
LENGTH: 773
  OTHER INFORMATION: plants

PUBLICATION INFORMATION:
AUTHORS: Strizhov, Nicolai, Keller, Menachem; Mathur, Jadeep;
AUTHORS: Strizhov, Nicolai, Keller, Menachem; Mathur, Jadeep;
AUTHORS: Koncz, Lim, Zsuzsanna, Bosch, Dirk; Prudovsky, Evgenia; Schell, AUTHORS: Jeff; Sneh, Baruch; Koncz, Csaba; Zilberstein, Aviah
TITLE: A synthetic cryIC gene, encoding a Bacillus thuringiensis
TITLE: k-endotoxin, confers Spodoptera resistance in alfalfa and tobacco JOURNAL: Proc. Natl. Acad. Sci. USA
VOLUME: 26
ISSUE: 26
PAGES: 15012 - 15017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCES CODING FOR POLYPEPTIDES ENDOWED WITH A LARVICIDAL ACTIVITY TOWARDS LEPIDOPTERA
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49.5%; Score 45; DB 4; Length 773;
Best Local Similarity 66.7%; Pred. No. 39;
Matches 10; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
49.5%; Score 45; DB 3; Length 630;
Best Local Similarity 53.8%; Pred. No. 31;
Matches 7; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                   ) PAGES: 15012 - 15017
; DATE: 24 - DEC - 1996
; RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 630
US-08-769-802A-2
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Sequence 2, Application US/08461551

Patent No. 579298

APPLICANT: SANCHIS, Vincent
APPLICANT: LEECLUS, Didier
APPLICANT: MARTOURET, Marguerite-Marie
APPLICANT: MARTOURET, Daniel
APPLICANT: MARTOURES: 2
CORRESPONDENCE ADDRESS: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: PO. Box 1404
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) ORGANISM: Acinetobacter baumannii
US-09-328-352-8203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261 LFSVFLRMLDENALP 275
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COUNTRY: USA
ZIP: 22313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-328-352-8203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
US-08-461-551-2
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us-10-092-750-48.rai
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Query Match 49.5%; Score 45; DB 3; Length 823; Best Local Similarity 53.8%; Pred. No. 42; Matches 7; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                   PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/461,551
FILING DATE: -CURROWN:
APPLICATION NUMBER: 05 07/458,754
FILING DATE: 10-DEC-1899
APPLICATION NUMBER: EP 88 401 121.4
FILING DATE: 06-MAY-1988
APPLICATION NUMBER: EP 88 401 121.4
FILING DATE: 10-UNJ-1987
ATTORNEY/AGETY INFORMATION:
NAME: HUNTINGTON, R. D.
REFIERPHOKE: (703) 836-6620
TELEPHOKE: (703) 836-6620
TELEPHOKE: (703) 836-6620
TELEPHOKE: (703) 836-6620
TELEPAX: (703) 836-2021
TELEFAX: (703) 836-620
TELEPAX: (703) 836-620
TELEPAX: (703) 836-621
SEQUENCE CHARACTERISTICS:
TELEFAX: (703) 836-620
TYPE: amino acid
STRANDENNESS: unknown
STRANDENNESS: unknown
WOLECULE TYPE: peptide
STRANDENNESS: unknown
US-09-037-621A-2
US-09-037-621A-2
TYPE: PEPTIDEN: SEQ ID NO: 2:
US-09-037-621A-2
TYPE: PEPTIDEN: SEQ ID NO: 2:
US-09-037-621A-2
TYPE: PARIOR CREATERION: SEQ ID NO: 2:
US-09-037-621A-2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,621A
FILING DATE: 10-MAZ-1998
CLASSIFICATION: <UNKNOWN>
11-DEC-1989
06-MAY-1988
10-JUN-1987
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Search completed: November 10, 2004, 14:55:36 Job time: 7.63868 secs

5 LLRYLADNFLPGG 17 |:::| ||:|| 41 LVQFLVSNFVPGG 53

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Gaps . 0

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Sequence

Sequence 10, Appl Sequence 59, Appl Sequence 61, Appl Sequence 6, Appli Sequence 2, Appli Sequence 10, Appli Sequence 61, Appli Sequence 14, Appli Sequence 1237, Appli Sequence 137, Appli Sequence 131, Appli

Run on:

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US-10-424-599-144449
US-10-425-115-218707
US-10-425-115-229739
US-10-425-114-64833
                  US-09-972-175-8
US-09-972-175-10
US-09-972-175-10
US-09-972-175-12
US-09-972-175-61
US-09-972-175-61
US-10-102-469-20
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US-10-200-522-4
US-10-200-522-8
US-10-200-522-10
US-10-200-522-10
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US-10-200-522-10
US-10-200-522-10
US-10-200-522-10
US-10-200-522-10
US-10-200-522-10
US-10-825-751-6
                                                                                                                                                                                                                                                                                                                                                  US-10-437-963-128149
US-09-837-961-4
                                                                                                                                                                                                                                            US-09-073-009-14
US-09-023-588-14
US-09-793-306-14
                                                                                                                                                                                                                                                                                                                                         US-09-922-683-10
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                                                                                                                                                                                      7
11
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Best Local Similarity 100.
Matches 18; Conservative
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11189
11189
1189
352
352
1189
1189
1189
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ORGANISM: Homo sapiens
US-10-092-750-48
 Sequence 48, Appl
Sequence 22, Appl
Sequence 4, Appli
Sequence 281976,
Sequence 273457,
Sequence 259841,
Sequence 37487,
Sequence 72803, A
Sequence 147749,
Sequence 2, Appli
Sequence 21, Appli
Sequence 21, Appli
                                                                             November 11, 2004, 01:28:30; Search time 20.8189 Seconds (without alignments) 305.399 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
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1: /cgn2 6/ptodata/1/pubpaa/Pcr_NEW PUB-COMB.pep:*

2: /cgn2 6/ptodata/1/pubpaa/Pcr_NEW PUB-pep:*

3: /cgn2 6/ptodata/1/pubpaa/Pcr_NEW PUB-pep:*

4: /cgn2 6/ptodata/1/pubpaa/USO6 NEW PUB.pep:*

5: /cgn2 6/ptodata/1/pubpaa/USO NEW PUB.pep:*

6: /cgn2 6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*

7: /cgn2 6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*

8: /cgn2 6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*

10: /cgn2 6/ptodata/1/pubpaa/USO8 PUBCOMB.pep:*

11: /cgn2 6/ptodata/1/pubpaa/USO8 PUBCOMB.pep:*

11: /cgn2 6/ptodata/1/pubpaa/USO9 NEW PUB.pep:*

11: /cgn2 6/ptodata/1/pubpaa/USO9 NEW PUB.pep:*

13: /cgn2 6/ptodata/1/pubpaa/USO9 NEW PUB.pep:*

14: /cgn2 6/ptodata/1/pubpaa/USO9 NEW PUB.pep:*

15: /cgn2 6/ptodata/1/pubpaa/USO00MB.pep:*

16: /cgn2 6/ptodata/1/pubpaa/USO10CPUBCOMB.pep:*

17: /cgn2 6/ptodata/1/pubpaa/USO10CPUBCOMB.pep:*

18: /cgn2 6/ptodata/1/pubpaa/USO10CPUBCOMB.pep:*

19: /cgn2 6/ptodata/1/pubpaa/USO10NB.pep:*

19: /cgn2 6/ptodata/1/pubpaa/USO10NB.pep:*

19: /cgn2 6/ptodata/1/pubpaa/USO0NB.pep:*

19: /cgn2 6/ptodata/1/pubpaa/USO0NB.pep:*

19: /cgn2 6/ptodata/1/pubpaa/USO0NB.pep:*

19: /cgn2 6/ptodata/1/pubpaa/USO0NB.pep:*

19: /cgn2 6/ptodata/1/pubpaa/USO0NB.pep:*
            GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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4 US-10-428-961-22

10S-10-424-524-4

7 US-10-425-115-281976

6 US-10-425-115-281976

6 US-10-425-114-37487

5 US-10-425-114-37487

5 US-10-425-114-7789

5 US-10-425-114-7789

6 US-09-918-485-2

10S-09-918-485-2

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Maximum Match 100%
Listing first 45 summaries
                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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91
1 LFSVLLRYLADNFLPGGS 18
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seq length: 200000000
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Match Length
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Perfect score:
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Maximum DB
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US-10-092-750-48

US-10-092-750-48

Sequence 48, Application US/10092750

PUDLICATION NO. US20030032157A1

GENERAL INFORMATION:
APPLICANT: Hammond, Philip W.
APPLICANT: Alpin, Julia
APPLICANT: Mright, Martin C.
TITLE OF INVENTION: Polypeptides Interactive with BCL-X1
FILE REPRENCE: 50036/050002
CURRENT FILING DATE: 2002-03-07

PRIOR APPLICATION NUMBER: US/10/092,750

CURRENT PLING DATE: 2001-03-08

NUMBER: OF SEQ ID NOS: 253

SOFTWARE: FestSEQ for Windows Version 4.0

SEQ ID NO 48

LENGTH: 18
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100.0%; Pred. No. 7.4e-08;
cive 0; Mismatches 0;
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US-10-428-961-22
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Result Š ·.

Gaps

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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Anount ic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Wu, Wei
APPLICANT: Burbaruk, Brad
APPLICANT: Burbaruk, Brad
APPLICANT: Burbaruk, Brad
APPLICANT: Burbaruk, Brad
APPLICANT: Barbaruk, Brad
APPLICANT: APPLICANTON: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: US/10/437,963
CURRENT APPLICANTON NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 173457
LENGTH: 318
Page 2

APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: 18-21(53222)B
CURRENT APPLICATION NUMBER: 105/10/425,115
CURRENT FILLING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 281976
LENGTH: 97
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Publication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Sou, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Can, Yihua
APPLICANT: Thou, Yihua
APPLICANT: Thou, Yihua
APPLICANT: Can, Yought
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17; Length 97;
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US-10-437-963-173457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
COTHER INFORMATION: Clone ID: MRT4577_20262C.1.pep US-10-425-115-281976
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Pred. No. 11;
0; Mismatches
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Best Local Similarity 81.8%;
Matches 9; Conservative
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ORGANISM: Oryza sativa
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US-10-437-963-173457
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                                                                                                                                                                APPLICANT: Baum, James A.
APPLICANT: Chu, Chih-Rei
APPLICANT: Chu, Chih-Rei
APPLICANT: Chonovan, William P.
APPLICANT: Glimer, Amy J.
APPLICANT: Glimer, Amy J.
APPLICANT: Rupar, Mark J.
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
FILE REFRENCE: MECO201-1,
CURRENT APPLICATION NUMBER: US/10/428,961
CURRENT FILING DATE: 2000-09-13
FRIOR PRIOR APPLICATION NUMBER: 60/53,995
PRIOR FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn version 3.2
SEQ ID NO 22

LENGTH: 1168
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APPLICANT: Boets, Annemie
APPLICANT: Boets, Annemie
APPLICANT: Boets, Annemie
APPLICANT: Boets, Annemie
APPLICANT: Damme, Nicole
APPLICANT: Machieu, Estijn
APPLICANT: Vanneste, Stijn
APPLICANT: NWBER: US/10/614,524
CURRENT FILING DATE: 2003-07-08
PRIOR APPLICATION NUMBER: US/09/739,243
PRIOR APPLICATION NUMBER: 60/173387
PRIOR APPLICATION NUMBER: 60/173387
PRIOR FILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 4
LENGTH: 1168
THENGTH: 1168
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Pred. No. 76;
4; Mismatches 1; Indels
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Pred. No.
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Publication No. US/20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/10614524 Publication No. US20040016020A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , ORGANISM: Bacillus thuringiensis US-10-428-961-22
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Best Local Similarity 61.5%;
Matches 8; Conservative
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Best Local Similarity 61.5%;
Matches 8; Conservative
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US-10-425-115-281976
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TITLE OF INVENTYON: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTYON: Plants and Uses Thereof for Plant Improvement

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STORREY FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128
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Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Liu, Jingdong

APPLICANT: Screen. Steven E

APPLICANT: Screen. Steven E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

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TITLE OF INVENTION: Nucleic Acid Molecules Acid Mith

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 46; DB 17; Length 619;
Pred. No. 82;
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US-10-425-114-37487
                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANIEM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_168593C.1.pep
US-10-425-115-259841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 259841
LENGTH: 619
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Best Local Similarity 52.9%;
Matches 9; Conservative
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
US-10-425-114-37487
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Sequence 147749, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Sorein, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabasfa, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
NUMBER OF SEQ ID NOS: 73128
SEQ ID NOS: 73128
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Pred. No. 82;
2; Mismatches 6; Indels
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50.5%; Score 46; DB 15; Length 622;
Best Local Similarity 52.9%; Pred. No. 82;
Matches 9; Conservative 2; Mismatches 6; Indels
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3632-026-F12_FLI.pep
US-10-425-114-60096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: LIB4702-003-B5_FLI.pep
US-10-425-114-72803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: unsure
LOCATION: (1)..(71)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-425-114-72803
Sequence 72803, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
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ilarity 52.9%;
Conservative
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 9; Conserv
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ORGANISM: Zea mays
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Fri Nov 12 14:55:32 2004

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Query Match

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APPLICANT: Stelman, Steven J.
APPLICANT: Stelman, Steven J.
APPLICANT: Stelman, Steven J.
APPLICANT: Stelman, Steven J.
APPLICANT: Narraw, Kennerbh E.
TILE OF INVENTYON: Plant-Optimized Genes Encoding Pesticidal Toxins
FILE REFERENCE: MA-714XC2D1
CURRENT APPLICATION NUMBER: US/09/826,660
CURRENT FILING DATE: 1098-10-23
PRIOR PILING DATE: 1998-10-23
PRIOR FILING DATE: 1998-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-03-02
NUMBER OF SEQ ID NOS: 2.0
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO. 21
LENGTH: 1163
TYPE: PRT
TYPE: PRT
                       Gaps
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Publication No. US20030101482A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GILMER, Amy Jelen
Mettus, Annewarie Light
Mettus, Annewarie Light
ITLE OF INVENTION: TRANSMENIC PLANTS EXPRESSING
LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1163;
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Pred. No. 2.3e+02;
4; Mismatches 2; Indels
                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/972,175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene US-09-826-660-21
  Pred. No. 1.6e+02;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 05-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                        Sequence 21, Application US/09826660 Patent No. US20010026940A1 GENERAL INFORMATION:
                            4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49.5%;
ilarity 53.8%;
Conservative
    53.8%;
                                                                       5 LLRYLADNFLPGG 17
                                                                                                    41 LVQFLVSNFVPGG 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 LLRYLADNFLPGG 17
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                            7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Texas
COUNTRY: USA
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Matches 7; Conserv
Best Local Similarity
Matches 7; Conserv
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Publication No. US20030115628A1
GENERAL INFORMATION:
APPLICANT: SANCHIS, Vincent
LERECLUS, Didier
MENOU, Ghislaine
LECADET, Marguerite-Marie
DEDONDER, Daniel
DEDONDER, Paymond
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR
LEPIDOPTERA
LEPIDOPTERA
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                                                                                                                                            Gaps
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0
                                                                                               Length 71;
                                                                                                                                          Indels
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MEDUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Fatentin FC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
       ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_104438C.1.pep
US-10-424-599-147749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS.
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. BOX 1404
                                                                                            Score 45; DB 15;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/918,485
FILING DATE: 25-OCC-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/461,551
FILING DATE: 05-UNN-1994
APPLICATION NUMBER: US 07/458,754
FILING DATE: 11-DEC-1989
APPLICATION NUMBER: EP 88 401 121.4
FILING DATE: 06-MXY-1988
APPLICATION NUMBER: EP 88 401 121.4
FILING DATE: 10-UNN-1987
ATTORNEY/ACTION NUMBER: FP 87 08090
FILING DATE: 06-MXY-1988
APPLICATION NUMBER: PP 87 08090
FILING DATE: 06-WXY-10-NUMBER: PP 87 08090
FILING DATE: 06-WXY-10-NUMBER: PP 87 08090
FILING DATE: 06-WXY-10-NUMBER: PP 87 08090
FILING DATE: 07-UNN-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: HUNTINGTON, R. D.
REGISTRATION NUMBER: 27,903
REFERENCE/DOCKET NUMBER: 010830-073
                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown;
MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-918-485-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEPAX: (703) 836-2021
INFORMATION FOR SEC ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 823 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: unknown
                                                                                            Query Match
Best Local Similarity 69.2%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Alexandria
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                       6 LRYLADNFLPGGS 18
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US-09-918-485-2
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Gaps
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Sequence 6, Application US/09972175
Publication No. US20030101482A1
GENERAL INFORMATION:
APPLICANT: Baum, James A.
Gilmer, Amy Jelen
Mettus, Anne-Marie Light
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
TITLE OF INVENTION: LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 45; DB 10; Length 1189;
Pred. No. 2.4e+02;
4; Mismatches 2; Indels
    Length 1189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORPATION SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/972,175
FILING DATE: 05-Oct-2001
CLASSIFICATION ACTORNOWD
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/337,635
FILING DATE: «UNKNOWD
ATTORNEY/AGENT INFORMATION:
Query Match
49.5%; Score 45; DB 10; Length 11
Best Local Similarity 53.8%; Pred. No. 2.4e+02;
Matches 7; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: November 11, 2004, 02:43:04 Job time : 21.8689 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ' TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-972-175-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEPAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
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41 LVQFLVSNFVPGG 53
                                                                                              5 LLRYLADNFLPGG 17
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Best Local Similarity 53.8
Matches 7; Conservative
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Sequence 4, Application US/09972175
Publication No. US20030101482A1
GENERAL INFORMATION:
APPLICANT: Baum, James A.
Gilmer, Amy Jelen
Mettus, Anne-Marie Light
TITLE OF INVENTION: TRANSCENIC PLANTS EXPRESSING
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 45; DB 10; Length 1189;
Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER REACTION TYPE: FLORDY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/972,175
FILING DATE: 05-Oct-2001
CLASSIFICATION: cunknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/337,635
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:206
                                                                      NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:206
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
RDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
;
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-972-175-4
                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
       APPLICATION NUMBER: 09/337,635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
                             FILING DATE: <Unknown:
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 512/474-7577
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                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 LLRYLADNFLPGG 17
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41 LVQFLVSNFVPGG 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Texas
COUNTRY: USA
                                                                                                                                                                                                                                                                               TYPE: amino
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US-09-972-175-4
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OM protein - protein search, using sw model

November 10, 2004, 13:40:53; Search time 4.41509 Seconds (without alignments) 392.268 Million cell updates/sec Run on:

US-10-092-750-48 91 1 LFSVLLRYLADNFLPGGS 18 BLOSUM62 Gapop 10.0 , Gapext 0.5 Perfect score: Scoring table: Sequence:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

ption	•	NADH flavin oxidor	-11	ica	protoxin - Bacillu	probable NADH-depe	parasporal crystal			й	-	3] C	parasporal crystal	probable RNA helic	probable helicase	probable ATP-bindi	hypothetical prote	prot	EG	ol49 protein - Esc	hypothetical prote	hypothetical prote	sucrose-phosphatas	conserved hypothet	glucose-1-phosphat	hypothetical prote	0	β	probable lipopolys
Ħ	AB1136	•	A75201		JC7			Н							C8612		T003	855669	T500	F651							G6467		G8198
DB	¦		2																										
ouery Match Length	664	99	570	57(	65	678	823	1106	118	473	268	116	116	2113	2113	238	94	1346	167	145	14	14	18.	316	326	386	613	613	623
Query Match	50.5		49.5					49.5			47.3	47.3	47.3	46.7	46.7	46.2	ė.	46.2	Ġ	45.1	ď.	45.1	45.1	45.1	45.1	45.1	45.1	45.1	45.1
Score	46	46	45	45	45	45	45	45	45	44	43	43	43	•	42.5	42	42	42	42	41	41	41	41	41	41	41	41	41	41
Result No.	1	8	m	4	ľŪ	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

ATP-dependent CLP	hypothetical prote	endopeptidase Clp	endopeptidase Clp	probable pre-tRNA	nad-specific gluta	parasporal crystal	multidrug resistan	BIR repeat contain	cutinase - fungus	sensor histidine k	hypothetical prote	glucose-1-phosphat	O-antigen polymera	glycerol trinitrat	hypothetical prote
F81396	C87358	AC2096	1000ND	T40803	T40931	A48970	T18279	T31067	S21427	H87561	G72778	T48866	A47677	AI3558	T26511
7	7	N	7	N	N	N	(7	0	Н	N	(7)	N	~	7	0
857	859	880	945	978	1106	1176	1743	4845	223	839	138	355	359	371	378
45.1	45.1	45.1	45.1	45.1	45.1	45.1	45.1	45.1	44.5	44.5	44.0	44.0	44.0	44.0	44.0
41	41	41	41	41	41	41	41	41	40.5	40.5	40	40	40	40	40
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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NADH flavin oxidoreductase homolog lmo0489 [imported] - Listeria monocytogenes (strain C'Species: Listeria monocytogenes C'Species: C'Speci
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A;Gene: 1mo0489 C;Superfamily: Methylophilus methylotrophus W3Al trimethylamine dehydrogenase

Gaps . 0 Query Match 50.5%; Score 46; DB 2; Length 664; Best Local Similarity 47.1%; Pred. No. 13; Matches 8; Conservative 4; Mismatches 5; Indels

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218 FPIVLRFSADEFTEGGN 234 2 FSVLLRYLADNFLPGGS 18 ð g

RESULT 2

AD1494
NADH flavin oxidoreductase homolog lin0492 [imported] - Listeria innocua (strain Clip11 C;Specise Listeria innocua
C;Accession: AD1494
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeckc
S; Doneinguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H
D; Jones, L.M.; Karst, U.
Science 244, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Fok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Scatus: preliminary
A;Scatus: preliminary
A;Residues: l-664 cGLA>
A;Residues: l-664 cGLA>
A;Cross-references: UNIPROT:Q92EG8; GB:AL592022; PIDN:CAC95724.1; PID:g16412932; GSPDB

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Query Match Best Loc Matches

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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: Thinan, Thin
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C;Species: Sinorhizobium meliloti
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: B95968
B;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Herna, Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-4kb pSymB megaplasmid from the N2-fixing end A;Reference number: A5842; MUD:21396508; PMID:11481431
                    NyAlternate names: crylC protein
C;Species: Bacillus thuringiensis
C;Datecies: Bacillus thuringiensis
C;Datecies: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 11-May-2000
C;Accession: UC7140
R;Christov, N.K.; Imaishi, H.; Ohkawa, H.
Biosci. Biotechnol. Biochem. 63, 1433-1444, 1999
A;Title: Green-tissue-specific expression of a reconstructed crylC gene encoding the present litura.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Genome: plasmid
C;Superfamily: Methylophilus methylotrophus W3Al trimethylamine dehydrogenase
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Pred. No. 19;
3; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: JC7140; MUID: 99430790; PMID: 10501003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 45; DB 2;
Pred. No. 18;
4; Mismatches 2
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C,Superfamily: parasporal crystal protein
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Best Local Similarity 52.9%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Molecule type: DNA
A,Residues: 1-655 <CHR>
A,Cross-references: EMBL:X96682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:::| ||:|||
41 LVQFLVSNFVPGG 53
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Best Local Similarity
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C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: H4-Mq2-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
C;Accession: E71234
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, Y.; Hino, Y.; Yamamoto, S.; Sekir
M; Ohltku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Hino, Y.; Yamamoto, S.; Sekir
M; Ohltku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Hino, Y.; Yamamoto, S.; Sekir
M; Ohltku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Hino, Y.; Yamamoto, S.; Sekir
DNA Res. S. 55-76, 1938
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Recession: E71234
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Accession: E71234
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Coss-references: UNIPROT:O57875; GB:AP000001; NID:g3236128; PIDN:BAA29204.1; PID:g325
A;Coss-references: UNIPROT:O57875; GB:AP000001; NID:g3236128; PIDN:BAA29204.1; PID:g325
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Gennetics:
A;Gene: PH0135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyaccesion: A75201
Ryanonymous, Genoscope sequence: insights into archaeal chromosome strukined to the EMBL Data Library, July 1999
A; Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome strukined to the EMBL a75001
A; Reference number: A75001
A; Accession: A75201
A; Amolecule type: DNA
A; Molecule type: DNA
A; Residues: 1-570 < KAN>
A; Coss-references: UNIPROT; Q9V2E2; GB: AJ248283; GB: AL096836; NID: G5457433; PIDN: CAB4905
A; Genetics:
A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: 
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                                                                                                   A;Gene: lin0492
C;Superfamily: Methylophilus methylotrophus W3A1 trimethylamine dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypotherical protein PAB0082 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
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Pred. No. 16;
1; Mismatches 1; Indels
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Pred. No. 16;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                          50.5%; Score 46; DB 2; Length 664; ilarity 47.1%; Pred. No. 13; Conservative 4; Mismatches 5; Indels
A, Experimental source: strain Clip11262 C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218 FPIVLRFSADEFTEGGN 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                2 FSVLLRYLADNFLPGGS 18
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Best Local Similarity 80.0
Matches 8; Conservative
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211 LRYLVENFLP 220
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Best Local Similarity
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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Sacession: F70513
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Reference number: A70500, MJ1D:98295987; PMID:9634230
A;Reference number: A70500, MJ1D:98295987; PMID:9634230
A;Reference number: A70500, MJ1D:98295987; PMID:9634230
A;Retus: pre-liminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 11-473 <COL>
A;Residues: 11-473 <COL>
A;Residues: 11-473 <COL>
A;Residues: Ereferences: GB:297559; GB:AL123456; NID:93261820; PIDN:CABI0718.1; PID:e328403
A;Resperimental source: strain H37Rv
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C;Species: Chlamydia trachomatis
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Ju1-2004
C;Accession: G71472
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchel.
Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trans.
A;Reference number: A71570; MUID:99000809; PMID:9784136
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C;Species: Bacillus thuringiensis
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S32647
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                   Mismatches
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Best Local Similarity 66.7
Matches 10; Conservative
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LLRFRKDSFLPG 234
                   7; Conservative
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A;Molecule type: DNA
A;Residues: 1-268 <ARN>
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les 8; Conserv
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               Matches
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R. Sammons, L.; Wohldmann, P.
Submitted to the EMBL Data Library, July 1997
A.Description: The Sequence of C. elegans cosmid C05C8.
A.Reference number: Z21078
A.Reference number: Z21078
A.Reference number: Z21078
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Residues: 1-1106 < SAM
A.Residues: 1-1106 < SAM
A.Residues: UNIPROT:016310; EMBL:AP016430; PIDN:AAB65371.1; GSPDB:GN00023; CESP:A.Experimental source: strain Bristol N2; clone C05C8
C; Accession: S04181
Mol. Microbiol. 50.7 Elecadet, M.M.
Mol. Microbiol. 3, 229-238, 1989
A; Title: Microbiol. 3, 229-238, 1989
A; Title: Nucleotide sequence and analysis of the N-terminal coding region of the Spodopt A; Reference number: S04181; MUD: 89343627; PMID: 2548060
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Cross-references: UNIPROT: P05518; EMBL: X13620; NID: 940355; PIDN: CAA31951.1; PID: 940356
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C.Species: Bacillus thuringiensis
C.Species: Bacillus thuringiensis
C.Species: Bacillus thuringiensis
C.Accession: 500944
R.Honee, G.; van der Salm, T.; Visser, B.
R.Honee, G.; van der Salm, T.; Visser, B
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Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
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A;Map position: 5
A;Introns: 25/3; 78/3; 117/1; 245/1; 591/1; 787/1; 1008/2
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Pred. No. 32;
1; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                       C; Superfamily: parasporal crystal protein C; Keywords: delta-endotoxin
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1 Similarity 55.6%;
10, Conservative
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Best Local Similarity 53.8%;
Matches 7; Conservative
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41 LVQFLVSNFVPGG 53
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Matches 10; Conserv
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R; Haysahi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. Basawara, B. 11-22, 2001
A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gend A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gend A; Reference number: A99629; MUID:21156231; PMID:11258796
A; Reference number: A99629; MUID:21156231; PMID:11258796
A; Residues: preliminary
A; Molecule type: DNA
A; Residues: 1-2113 cHAY
A; Residues: 1-2113 cHAY
A; Residues: UNIPROT:Q8XC71; GB:BA000007; PIDN:BAB38686.1; PID:g13364741; GSPDB:GCGenetics:
C; Genetics: A; Gene: EC55263
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R;Hoeffer, H.; Soetaert, P.; Jansens, S.; Peferoen, M.

Nucleic Acids Res. 18, 5545, 1990

A;Title: Nucleotide sequence and deduced amino acid sequence of a new Lepidoptera-specif

A;Reference number: S11446

A;Reference number: S11446

A;Residue: preliminary

A;Molecule type: DNA

A;Residues: 1-1165 cHOB.

A;Residues: 1-1165 cHOB.

A;Cross-references: UNIPROT:P19415; EMBL:X54160; NID:g40279; PIDN:CAA38099.1; PID:g40280

C;Superfamily: parasporal crystal protein

C;Keywords: delta-endotoxin
         R;Lambert, B.
submitted to the EMBL Data Library, April 1993
A;Reference number: $32645
A;Reference number: $32645
A;Accession: $32647
A;Accession: $32647
A;Residue: preliminary
A;Residues: 1-1160 < LAM>
A;Residues: 1-1160 < LAM>
Cross-references: UNTROT: Q45747; EMBL: 222511; NID: 9295863; PIDN: CAA80234.1; PID: 92958
C;Superfamily: parasporal crystal protein
C;Reywords: delta-endotoxin
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C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
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Alalternate names: parasporal crystal protein crylD
C;Species: Bacillus thuringiensis
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
47.3%; Score 43; DB 2; Length 1165;
Best Local Similarity 53.8%; Pred. No. 73;
Matches 7; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                               Score 43; DB 2; Length [160; Pred. No. 73; 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |: :| ||:|||
41 LINFLYSNFVPGG 53
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41 LINFLYSNFVPGG 53
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Best Local Similarity
Matches 10; Conserv
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2 FSVLLRYLADNFLPGG 17

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C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Dates: 10-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: G6D-28
R;Perna, N. T.; Plunket III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayher iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca Aytitle: Genome sequence of enterchemorrhagic Escherichia coli 0157:H7.
probable helicase Z5901 [imported] - Escherichia coli (strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                     A;Accession: CB6128
A;Status: preliminary
A;Mocession: CB6128
A;Status: preliminary
A;Mocession: Dreliminary
A;Mocession: 1-2113 <8TO>
A;Cross-references: UNIPROT:Q8XC71; GB:AE005174; NID:g12519309; PIDN:AAG59487.1; GSPDB:A;Rycatimental source: strain O157:H7, substrain BDL933
C;Genetics:
A;Gene: ZS901
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46.7%; Score 42.5; DB 2;
Best Local Similarity 62.5%; Pred. No. 1.7e+02;
Matches 10; Conservative 2; Mismatches 1;
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POSSIB bacillus the Moyneb bacillus the Agmo0264 bacillus the Agmo17362 bacillus Agmo17362 bacillus opserved mycobacteric and mycobacteric and anopheles gover anopheles gover

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STRAIN=R3;
Li M.S., Choi J.Y., Roh J.Y., Shim H.J., Boo K.S., Je Y.H.;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AX570738; AA693799.1; -.
InterPro; IPR001178; Endotoxin.
InterPro; IPR005639; endotoxin.
InterPro; IPR005639; endotoxin.
InterPro; IPR005639; endotoxin.
InterPro; IPR008979; Gal bind like.
Fram; PF003944; Endotoxin.
Fram; PF003945; Endotoxin.
Fram; PF03945; Endotoxin.
Fram; Fram; FF03945; Endotoxin.
FF03945; Endotoxi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=K3;
Li M.S., Choi J.Y., Roh J.Y., Shim H.J., Boo K.S., Je Y.H.;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AYS70736; AAS93799.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 48; DB 2; Length 782;
Pred. No. 39;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS93799;
26-ARR-2004 (TrEMBLrel. 27, Created)
26-ARR-2004 (TrEMBLrel. 27, Last sequence update)
26-ARR-2004 (TrEMBLrel. 27, Last sequence update)
26-ARR-2004 (TrEMBLrel. 27, Last annotation update)
Cryl type crystal protein (Fragment).
Bacillus thuringiensis (subsp. kenyae).
Bacillus cereus group; Bacillales; Bacillus;
Bacillus cereus group; Bacillus thuringiensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Cryl type crystal protein (Fragment).
Bacillus thuringiensis (subsp. kenyae).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89009 MW; 36990BD477860DB9 CRC64;
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                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
C1CA_BACTE
Q9L877
AAM00264
AAL79362
Q9BMQ3
Q6DFM3
Q6DFM3
Q7VEG6
Q79FH3
CAE55457
Q70063
CAE55457
CYNDW2
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Best Local Similarity 61...
Best Mach Similarity 61...
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LLOFLLNNFVPGG 47
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  782 AA;
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  782
    SEQUENCE
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QEPYW6
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ID AAS9

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A893799 bacillus th
Q45716 bacillus th
Q45716 bacillus th
Q23676 arabidopsis
Q39046 arabidopsis
Q39047 arabidopsis
Q32az6 bacillus th
Q8pib5 azotobacter
Q8pz1 bradyrhizob
Q7wt25 streptomyce
Q7wt25 streptomyce
Q7wt25 streptomyce
Q723g0 listeria mo
Q723g1 listeria mo
Q802eg bovine herp
Aar86131 bovine herp
Aar86131 bovine herp
Q662x7 bartonella
Q662x7 bartonella
Q662x7 bartonella
Q662x7 bartonella
Q8141 pyrococcus
Q8141 pyrococcus
Q8141 pyrococcus
Q8145 pyracoccus
Q8145 pyracoccus
Q8141 pyrococcus
                                                                                                                            November 10, 2004, 13:38:57; Search time 23.9774 Seconds (without alignments) 431.938 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                  5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                             hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                         1825181 segs, 575374646 residues
                  GenCore version (c) 1993 - 2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS93799
CLUA BACTU
CLUB BACTU
023678
039046
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CLGB BACTZ
08GHE8
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Maximum Match 100%
Listing first 45 summaries
                                                                                              sw model
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AAR86131
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AAT03301
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Q7WT25
Q7MBG3
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Q8H633
O57875
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Q6FEW8
Q8IDF9
O16310
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089604
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Q8U4L1
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                        1 LFSVLLRYLADNFLPGGS 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                              OM protein - protein search, using
                                                                                                                                                                                                                                                                                                                                                                                                                                     seq length: 0
seq length: 200000000
                                                                                                                                                                                                                US-10-092-750-48
91
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Match Length DB
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11167
11167
11169
6022
622
11169
280
282
354
606
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11246
11246
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Perfect score:
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Maximum DB
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
             30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 34, Last sequence update)
65-UJL-2004 (Rel. 44, Last annotation update)
Pesticidial crystal protein crylub (Insecticidal delta-endotoxin
Crylu(b)) (Crystaline entomocidal protexin) (134 kDa crystal protein).
Name=crylub; Synonyms=crylu(b), cryEfl;
Bacillus thuringiensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                     lepidopteran insects.";
Patent number US5356623, 18-OCT-1994.
-!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut
epithelial cells of many lepidopteran larvae. Toxic to Plutella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the spore coat.
                                                                                                                                                                                                                                                                                                                                                                                                                                            sporulation and is accumulated both as an inclusion and as part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Federspiel N.A., Conway A.B., Conway A.R., Davis K., Brendel V.,
                                                                                                                                                                                                                                                                                                                                                                                                                            DEVELOPMENTAL STAGE: The crystal protein is produced during
                                                                                                                                                                                                                                SEQUENCE FROM N.A. STADSDAL, SESSO92; STRANSINEL B-18973 / EGSO92; VOD Tersch M.A., Gonzalez J.M. Jr.; Bacillus thuringiensis cryET1 toxin gene and protein toxic to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 1170;
59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sporulation; Toxin.
SEQUENCE 1170 AA; 133553 MW; B053B9619B78DC19 CRC64;
                                                                                                                                                           Bacteria; Firmičutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Belongs to the delta endotoxin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
CER1-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin.C.
InterPro; IPR005639; endotoxin.C.
InterPro; IPR008979; Gal bind Ilke.
Pfam; PF03944; Endotoxin.C; 1.
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HSSP; P02965; 1CIY.
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LLQFLLNNFVPGG 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                     NCBI_TaxID=1428;
                                                                                                                                                                                                                                                                                                                                                                                                        xylostella.
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                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2004 (Rel. 44, Last annotation update)
Pesticidial crystal protein crylla (Insecticidal delta-endotoxin.
Cryll(a)) (Crystaline entomocidal protoxin) (133 kDa crystal protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sporulation and is accumulated both as an inclusion and as part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=NRRL B-21110 / EG5847;
Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;
Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;
Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;
Bactlus thuringiensis cryst4 and cryet5 toxin genes and proteins
toxic to lepidopteran insects.";
Patent number U55322687, 21-4UN-1994.
Patent number U55322687, 21-4UN-1994.
-!- FUNCTION: Promotes Colloidosmociic lysis by binding to the midgut
epithelial cells of many lepidopteran larvae.
-!- DEVELOPMENTAL STAGE: The crystal protein is produced during
                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the spore coat.
-!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
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                                                           Score 48; DB 2; Length 782;
Pred. No. 39;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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REGHENCE 1167 AA; 132760 MW; 3B7357D14E655FC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Belongs to the delta endotoxin family.
                    89009 MW; 36990BD477860DB9 CRC64;
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Pred. No. 59;
4; Mismatches
                                                                                                                                                                                                                                                                                                   PRT; 1167 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=crylJa; Synonyms=crylJ(a), cryET4;
Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001176; Endotoxin.
InterPro; IPR005639; endotoxin.
InterPro; IPR005639; endotoxin.N.
InterPro; IPR008979; Gal_bind_like.
Pfam; PF03944; Endotoxin_N.
Pfam; PF03945; Endotoxin_M; I.
Pfam; PF03945; Endotoxin_N; I.
                                                             52.7%;
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Best Local Similarity 61.5%;
Matches 8; Conservative
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HSSP; P02965; 1CIY.
                                           Query Match
Best Local Similarity 61.5-
Local Similarity 61.5-
Local Similarity 61.5-
Local Similarity 61.5-
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782 AA;
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Q45738;
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ClJB_BACTU
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NCBI_TaxID=3702;
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Deng M.D., Peng S., Lemieux B.;

Menomic (Accession No. X95964) and cDNA (Accession No. X95965)

sequences of the CER1-like gene of Arabidopsis thaliana derived from a plant DNA/T-DNA insertion junction. (PGR96-019).";

Plant Physiol. 110:1436-1436(1996).
Palm C.J., Au M., Araujo R., Chung E., Kurtz D.B., Buehler B., Dewar K., Feng J., Kim C., Li Y., Shinn P., Sun H., Oji O., Osborne B., Shen Y.K., Toriumi M., Vyotskaia V., Yu G., Theologis A., Ecker J., Davis R.W.,
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, 189959; AACA4373.1; -.
GO; GO:0008152; P:netabolism; IEA.
InterPro; IPR006087; Sterol desat.
InterPro; IPR006088; Sterol desat.
InterPro; IPR006088; Sterol desat.
SEQUENCE 604 AA; 69334 MW; BOC46279AA473782 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
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Pred. No. 46;
                                                                                                                            Score 47; DB 2;
Pred. No. 44;
                                                                                                                                                                                                                                       622 AA
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55.6%;
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-OCT_2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2003 (TrEMBLrel. 25,
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Best Local Similarity 55.6.
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Best Local Similarity 55.6
Matches 10; Conservative
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Name=CER1-like;
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Name=CER1-like;
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Q39047
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its work by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Deng M.D., Peng S., Lemieux B.;

Sequences of the CER1-like gene of Arabidopsis thaliana derived from a plant DNA/T-DNA insertion junction. (PGR96-019).";

Plant DNA/T-DNA insertion junction. (PGR96-019).";

EMBL; X95965; CAR65200.1; -

GO; GO:0003824; R:catalytic activity; IEA.

GO; GO:000152; P:metabolism; IEA.

GO; GO:0008152; P:metabolism; IEA.

InterPro; IPR006089; Sterol_desat.

InterPro; IPR006089; Sterol_desat.

ERQUENCE 623 AA; 71571 MW; BD896FP94EC5718C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 wuhanensis strain.";
Curr. Microbiol. 40.227-232(2000).
-!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut
-!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut
-!- DEVELOPMENTAL STAGE: The crystal protein is produced during
sporulation and is accumulated both as an inclusion and as part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Pesticidial crystal protein crylGP (Insecticidal delta-endotoxin
CryIG(b)) (Crystaline entomocidal protoxin) (133 kDa crystal protein)
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MEDLINE=20153386, PubMed=10688690;
Kuo W.-S., Lin J.-H., Tzeng C.-C., Kao S.-S., Chak K.-F.,
"Cloning of two new cry genes from Bacillus thuringiensis subsp.
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=52024;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 47; DB;
Pred. No. 46;
3; Mismatches
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Interpro; IPR005638; endotoxin.
Interpro; IPR005639; endotoxin N.
Interpro; IPR008979; Gal_bind_like.
Pfam; PP03944; Endotoxin C; 1.
Pfam; PP03945; Endotoxin M; 1.
Pfam; PP03945; Endotoxin M; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.6%;
55.6%;
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Best Local Similarity 55.6
Matches 10; Conservative
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MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces sp. AM-7161.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
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50.5%; Score 46; DB 2; Length 280; ilarity 60.0%; Pred. No. 30; Conservative 3; Mismatches 3; Indels
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SEQUENCE 282 AA; 30199 MW; 1AFE04BB6512BDF4 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                     282 AA.
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                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABC transporter permease protein.
OrderedLocusNames=blr3339;
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211 VFRVLLRYLSDREVP 225
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185 FSVVLRFLLPNILP 198
                                                                                                                             1 LFSVLLRYLADNFLP 15
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      Query Match
Best Local Similarity
Matches 9; Conserv
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hes 9; Conserv
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SEQUENCE FROM N.A.
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01-JUN-2003
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SEMBL, AF237388; AAR739511; -. SEQUENCE .. S
                                                                                                                                Gaps
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Azoteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Azotobacter.
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Pred. No. 87;
3; Mismatches 3; Indels
                                                              Score 47; DB 1; Length 1169;
Pred. No. 87;
                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1169 AA; 132990 MW; 07C9D6D180F3DB6D CRC64;
               1169 AA; 132904 MW; DIEFC1508A8B10BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus thuringiensis.
Bacteria, Firmicutes; Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=1428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Li C., Zhang J., Li G., Huang D.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF288683; AAO13756.1; -.
HSSP; P02965; ICIY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ol-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Last annotation update)
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                                                                                                                                   3; Mismatches
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InterPro; IPRO05638; endotoxin.C.

InterPro; IPRO05639; endotoxin.N.

InterPro; IPRO08979; Gal. bind. Tike.

Pfam; PPO0555; Endotoxin.C; I.
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Local Similarity 57.1%;
les 8, Conservative
                                                                    51.6%;
Similarity 57.1%;
8; Conservative
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40 ITRLILENFLPGGS 53
                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                       Query Match
Best Local Similarity
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STRAIN=B-Pr-88;
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Name=ampE;
                  SEQUENCE
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Best Local
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Q8GHE8
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Gaps

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184 VILPYLARGFLDGGS 198

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disear P., Frangeul L., Bucherieser C., Rusnick C., Amend A.,
Adlaser P., Frangeul L., Bucher H., Brandt P., Chakraborty T.,
Adrabit A., Chetouani F., Couve B., de Darnvar A., Dehoux P.,
Domann B., Dominguez-Bernal G., Duchaud B., Durant L., Dussurget O.,
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Adutier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Mattournah A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Comparative genomics of Listeria species.";
Comparative genomics of Listeria species.";
Electron 294:849-852(2001).
Electron 294:849-852(2001).
Electron 294:849-852(2001).
Electron 294:849-852(2001).
Electron 294:849-852(2001).
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R HISSP; PAT1278; AUG92;

Listilist; LIN0492;

GO; GO:000518; P:electron transport; IEA.

GO; GO:000518; P:electron transport; IEA.

R GO; GO:000518; P:electron transport; IEA.

R InterPro; IPR00132; PAD_DY_redox.

R InterPro; IPR00135; PAD_DY_redox.

R InterPro; IPR001155; Oxidored FMN.

R InterPro; IPR001155; Oxidored FMN.

R Pfam; PF00724; Oxidored FMN.

R PFINTS; PR00419; ADXRDTASE.

R PRINTS; PR00469; PADXRDTASE.

R PRINTS; PR00469; PADXRDTASE.

R ProDom; PD000139; FAD_DNR.

R ProDom; PD000139; FAD_DNR.

Complete proteone; FAD_; Flavoprotein; Oxidoreductase.

SEQUENCE 664 AA; 72912 MW; 57CA1857181B205D CRC64;
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                                                                                                                                                                                                                                                                                                                                                               Listeria innocua.
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
NCBI_TaxID=1642;
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Listeria monocytogenes.
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
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Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                          Created)
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STRAIN-CLIP 11262 / Serovar 6a;
MEDLINE-21537279; PubMed=11679669;
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FPIVLRFSADEFTEGGN 234
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                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2004 (TrEMBLrel. 26,
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                                                                                                                                                                                                                                                                                                                                    OrderedLocusNames=lin0492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                PRELIMINARY;
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Les 8; Conserv
                                                                                                                                                                                                                                                                                                               Lin0492 protein.
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                                                                                                          RESULT 14
Q92EG8
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RC STRAIN=AM-7161;

RX MEDLINE=22739559; PubMed=12855716;

RI Chinose K., Ozawa M., Irou K., Kunieda K., Ebizuka Y.;

RT Cloning, sequencing and heterologous expression of the medermycin biosynthetic gene cluster of Streptomyces sp. AM-7161: towards

RT comparative analysis of the benzolsochromanequione gene clusters.";

R. Microbiology 149:1633-1645(2003)

C. - CATALYTIC ACTIVITY: dTTP + alpha-D-glucose 1-phosphate = diphosphate + dTDP-glucose.

C. - SIMILARITY: Belongs to the glucose-1-phosphate

CC +1 SIMILARITY: Belongs to the glucose-1-phosphate

CC +1 SIMILARITY: Belongs to the glucose-1-phosphate

CC CC Htymidylyltransferase family.

EMBL; ABIO3463; BAC79029.1;

EMBL; ABIO3463; BATD-cransferase.

DR GO: 0017000; Prantibiotic biosynthesis; IRA.

INTERPRO; IPR005835; NTP-transferase.

ENTERPRO; IPR005835; NTP-transferase.

ENTERPRO; IRR05835; NTP-transferase.

ENTERPRO; IRR05037; MTA-INANGERSE.

ENTERPRO; IRR05037; MTA-INANGERSE.

ENTERPRO; IRR06103; MTA-INANGERSE.

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MEDLINE-22828889; PubMed=14500908;

Baar C., Eppinger M., Raddatz G., Simon J., Lanz C., Klimmek O.,

Nandakunar R., Gross R., Rosinus A., Keller H., Jagtap P., Linke B.,

Myer F., Lederer H., Schuster S.C.;

"Complete genome sequence and analysis of Wolinella succinogenes.";

Froc. Natl. Acad. Sci. U.S.A. 100:11690-11695 (2003).

EMBL; BX571662; CAEILI83.1;

RO; GO:0004066; Frasparagine synthase (glutamine-hydrolyzing). .; IEA.

RO; GO:0016874; F:ligase activity; IEA.

RO; GO:0004529; P:metabolism; IEA.

RO; GO:0008152; P:metabolism; IEA.

InterPro; IPR001962; Asn. Synthase.

InterPro; IPR006483; GATase.2.

Refam; PF00733; Asn. Synthase.2.

Refam; PF007319; GATase.2; 1.
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Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
Helicobacteracea, Wolinella.
NCBI_TaxID=844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
PUTATIVE ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZ (EC 6.3.5.4).
Name-PAB1605; OrderedLocusNames-WS2192;
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Pred. No. 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGRFAMS; TIGR01536; āsn_synth_AEB; 1.
PROSITE; PS00443; GATASE_TYPE_II; UNKNOWN_1.
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SEQUENCE 606 AA; 71101
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hes 8; Conservative
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STRAIN=DSMZ
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Query Match

Best Loc Matches

ઠ g Q7MBG3 Q7MBG3;

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RESULT 13 Q7MBG3 Gaps ö

NCBI\_TaxID=1639;

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REDINE=21537279; PubMed=11679669;

Redine=215, Berche P., Blocker H., Brandt P., Chakraborty T.,

Redine=21537279; PubMed=1167; Redine=2150 Purant L., Dussurget O.,

Redine=215, Redine=2167, Redine=2167; Redine
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Best Local Similarity 47.1%; Pred. No. 72;
Matches 8; Conservative 4; Mismatches 5; Indels
                                                    SEQUENCE FROM N.A.
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Search completed: November 10, 2004, 14:50:06 Job time : 25.9774 secs

| ::||: || | ||: 218 FPIVLRFSADEFTEGGN 234 2 FSVLLRYLADNFLPGGS 18

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Scoring table:

Searched:

Perfect score:

Seguence:

OM protein

Run on:

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Sequence 24, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 31076, A
Sequence 700, Appl
Sequence 7660, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 10, Appl
Sequence 11, Appl
Sequence 119, Appl
 Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.6%; Score 46.5; DB 4; Length 55; S8.8%; Pred. No. 2.3; tive 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                  Sequence 6534, Application US/09621976

Patent No. 663963

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENEET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
TENDER OF SEQ ID NOS: 19335
SEQ ID NO 6534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6991, Application US/09621976
Patent No. 6639053
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Goott, S.
APPLICANT: Goott, S.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOUTHARE: Patent.pm
SEQ ID NO 6991
LENGTH: 55
US-09-620-412C-245
US-09-620-412C-245
US-09-489-039A-13022
US-08-464-517-24
US-08-463-177-24
US-08-463-177-24
US-09-491-577-70
US-09-113-17-70
US-09-113-17-70
US-09-113-17-70
US-09-113-17-70
US-09-113-17-70
US-09-113-17-70
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US-09-113-70
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                                                                                                                                                                                                                                                                                     ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 WOVLLGKLLWKID-NPG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | || :| || || || || || wsqllrrlrwkddlnpg 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 58.8'8
Marches 10; Conservative
   ; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-6534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
US-09-621-976-6991
   RESULT 1
US-09-621-976-6534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-621-976-6991
   Query Match
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                                                                                                 November 10, 2004, 13:44:14; Search time 6.58868 Seconds (without alignments)
181.178 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                   Issued Patents AA:*

/ Ggn2 = 6/ptodata/1/iaa/5B_COMB.pep:*
/ Ggn2 = 6/ptodata/1/iaa/5B_COMB.pep:*
/ Ggn2 = 6/ptodata/1/iaa/6A_COMB.pep:*
/ Ggn2 = 6/ptodata/1/iaa/6A_COMB.pep:*
/ Ggn2 = 6/ptodata/1/iaa/PCTUS_COMB.pep:*
/ Ggn2 = 6/ptodata/1/iaa/PCTUS_COMB.pep:*
/ Ggn2 = 6/ptodata/1/iaa/PGTUS_COMB.pep:*
                GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-621-976-6534

US-09-621-976-6991

US-09-624-6812-7788

US-08-464-517-6

US-08-464-517-6

US-08-464-517-23

US-08-464-517-23

US-08-246-3613-6

US-08-246-3613-23

US-08-246-3613-23

US-08-246-3613-23

US-08-26-877-246

US-09-556-877-246

US-09-556-877-247

US-09-556-877-247

US-09-556-877-247

US-09-556-877-247

US-09-556-877-247

US-09-598-419-247

US-09-511-9990-7713

US-08-26-3613-50

US-08-26-3613-50

US-08-26-3613-50

US-08-26-571-12

US-08-26-571-12
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                                                                                                                                                                                                                                                           478139 seqs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                     sw model
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1 DWQVLLGKLLWKIDNPGI 18
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Gapop 10.0 , Gapext 0.5
                                                                       using
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Maximum DB seg length: 200000000
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Score

Result No.

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                                                                                                                                                                                                                Query Match

44.6%; Score 45.5; DB 2; Length 280;
Best Local Similarity 64.3%; Pred. No. 20;
Matches 9; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08463772

Sequence 6, Application US/08463772

GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESSS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CHY: Descon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

44.6%; Score 45.5; DB 3; Length 280;
Best Local Similarity 64.3%; Pred. No. 20;

Matches 9; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION 1435
PRIOR APPLICATION 10ATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-07-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: MALTHEW P. VINCENT
REGISTRATION NUMBER: 36,709
REGISTRATION NUMBER: 36,709
REPERSICE/DOCKET NUMBER: 36,709
REPERSICE/DOCKET NUMBER: MII-004C
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7400
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: MA
COUNTRY: USA
ZID. 102109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURENT APPLICATION NUMBER: US/08/463,772
TELECOMMUNICATION INFORMATION:
TELEPRONE: (617) 227-7400
TELEPRAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 DWEVLVLGKLKWDL 140
                                                                                                 1: 280 amino acids
amino acid
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                                                                                                                                 MOLECULE TYPE: protein US-08-464-517-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-463-772-6
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                                                                                                                                                                                                                                     APPLICANT: GARY BRETON:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7788
LENGTH: 189
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                           Gaps
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                           5; Indels
      Best Local Similarity 58.8%; Pred. No. 2.3;
Matches 10; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRICA APPLICATION 435
PRICA APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRICA APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
                                                                                                                                                                                               Sequence 7788, Application US/09543681A
Patent No. 6605709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 02109
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DW-----QVLLGKLLWKIDNPG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 DWFHMIPAVLLGSLLPDLDHPG 52
                                                              2 WOVILGKILWKID-NPG 17
                                                                                         20 WSQLLRRLRWKDDLNPG 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT; ORGANISM: Proteus mirabilis
US-09-543-681A-7788
                                                                                                                                                                                   US-09-543-681A-7788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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| Sequence 6. Application US/08246361A | Sequence 6. Application US/08246361A | Patent No. 599652 | GENERAL INFORMATION: APPLICANT: BEACH, David H. | TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50 | CORRESONDENCE ADDRESS: LAAIVE & COCKFIELD | STREET: 60 State Street | CITY: Boston | STATE: MA 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

44.6%; Score 45.5; DB 2;
Best Local Similarity 64.3%; Pred. No. 20;
Matches 9; Conservative 2; Mismatches 2;
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COUNTRY: USA
COUNTRY: USA
COUNTRY: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-MAY-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-CCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,708
FILING DATE: 26-MAY-1997
FILING DATE: 16-CCT-1992
PRIOR APPLICATION NUMBER: US 07/983,708
FILING DATE: 16-MAY-1991
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
                           CARANT AFFLICATION NAMES: US/08/464,517
FILING DATE:
CLASSIPICATION NAMES: US/08/464,517
FILING DATE: 16-0CT-1992
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-0CT-1992
APPLICATION NUMBER: US 07/01,514
FILING DATE: 16-MAY-1991
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
APPLICATION NUMBER: US 07/01,514
FILING DATE: 16-MAY-1991
APPLICATION NUMBER: MII-004C
RESISTRATION NUMBER: MII-004C
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 292 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||:|| |||| :
139 DWEVLVLGKLKWDL 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: peptide US-08-464-517-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-246-361A-6
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                                                                                                                                                                          Sequence 6. Sequence 7. Sequence 7. INVENTION: D-Type Cyclin and Uses Related Thereto NUMBER 0F SEQUENCES: 42. CORRESPONDENCE ADDRESS: 5. Sequence 7. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 23, Application US/08464517

Patent No. 5669640

GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 291;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

APPLICATION NUMBER: PCT/US93/05000

FILING DATE: 19930225

CLASSIFICATION NUMBER: US/07/888,178

FILING DATE: CAMY-1992

ATTORNEY/AGENT INFORMATION:

NAME: GRANATION NUMBER: 32,27

REFRENCE/DOCKET NUMBER: CSHL91-02A

TELEPHONE: 61-661-9540

INFORMATION FOR SEQ ID NO: 6: SEQUENCE: CHARACTERISTICS:

LENGTH: 291 amino acids

TYPE: AMINO ACID

TYPE: AMINO ACID

TELEPHOR ADDITED

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 45.5;
Pred. No. 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: BOSTON
STATE: MA
COUNTY: USA
ZIP: 021.09
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.6%;
127 DWEVLVLGKLKWDL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 DWEVLVLGKLKWDL 151
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Best Local Similarity 64.3%
...hes 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
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US-08-464-517-23
                                                                                                                                                                      PCT-US93-05000-6
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                                                                                                                            RESULT 6
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Sequence 23, Application US/08463772

Patent No. 6066501

GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKPIELD
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3; Length 292;
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GENERAL INFORMATION:
APPLICANT: MITOTIX
TITLE OF INVENTION: D-Type Cyclin and Uses Related Thereto NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11arity 64.3%; Score 45.5; I clarity 64.3%; Pred. No. 20; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION 100 DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-WAX-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-WAX-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE FOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: ASCIII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02109
CONFUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 23:
                                                                 139 bwevivickikwor 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 292 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DWOVL-LGKLLWKI 13
                           1 DWQVL-LGKLLWKI 13
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Best Local Similarity
Matches 9; Conserv
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PCT-US93-05000-23
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; Sequence 23, Application US/08246361A
; Patent No. 5998522
; GENERAL INFORMATION:
    APPLICANT: BEACH, David H.
    TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
    NUMBER OF SEQUENCES: 50
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: LAHIVE & COCKFIELD
    STREET: GO State Street
    CITY: Boston
    STREE MA
    STATE: WA
    COUNTRY: USA
    COUNTRY: USA
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44.6%; Score 45.5; DB 2; Length 292;
Best Local Similarity 64.3%; Pred. No. 20;
Matches 9; Conservative 2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-MAY-1994
CLASSIFICATION 435
PRIOR APPLICATION HAS
PELICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
RECOR APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION NUMBER: US 07/811
APPLICATION NUMBER: US 07/811
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 292 amino acids
       MII-004C
REFERENCE/DOCKET NUMBER: MITTELECOMOUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE: CHARACTERISTICS:
LENGTH: 292 amino acids
TYPE: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 64.3%;
Matches 9; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                  139 DWEVLVLGKLKWDL 152
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TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                         1 DWQVL-LGKLLWKI 13
                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-246-361A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: peptide US-08-246-361A-23
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Gaps

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Gaps
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| Sequence 246, Application US/09620412C
| Patent No. 6448234
| GENERAL INFORMATION:
| APPLICANT: Steven C. Pring
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
| TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
| FILE REFERENCE: 210121.46907;
| CURRENT APPLICATION NUMBER: US/09/620,412C
| CURRENT FILLING DATE: 2000-07-20
| NUMBER OF SEQ ID NOS: 363
| SOFTWARE: FastSEQ for Windows Version 3.0/4.0
| SEQ ID NO 246
| LEATH: 20
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Patent No. 6448234
GENERAL INFORMATION:
A APPLICANT: Steven P. Fling
ITILE OF INVENTION:
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 45; DB 4; Length 20;
Pred. No. 1.4;
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                US-09-556-877-247

Sequence 247, Application US/09556877

Patent No. 6432916

GARDERAL INNORMATION:
APPLICANT: Probst, Peter
APPLICANT: Bhatia, Ajay
APPLICANT: Ring, Steve
APPLICANT: Misonneuve, Jeff
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: COMPOSITIONS OF CHLAMYDIAL INPEC
FILE REFRENCE: 210121.469C5
CURRENT APPLICATION NUMBER: US/09/556,877

CURRENT FILING DATE: 2000-04-19

NUMBER OF SEQ ID NOS: 305

SEQ ID NOS: 305

SEQ ID NO 247

LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Made in a lab US-09-620-412C-246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ), OTHER INFORMATION: Made in a lab
US-09-556-877-247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 72.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 72.7
Matches 8; Conservative
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US-09-620-412C-246
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US-09-620-412C-247
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US-09-556-877-246
is Sequence 246. Application US/09556877
is Sequence 246. Application US/09556877
is Patent No. 643210.
is GENERAL INFORMATION:
APPLICANT: Probst, Peter
APPLICANT: Skaixy, Yasir
APPLICANT: Ring, Steve
APPLICANT: Maisonneuve, Jeff
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: COMPOSITIONS AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
TITLE OF SERENCE: 210121.46905.
CURRENT APPLICATION NUMBER: US/09/556,877
CURRENT FILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 305
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 246
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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Pred. No. 1.4;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISN PC compatible
COMPUTER: ISN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05000
FILING DATE: 19930525
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 45.5; D
Pred. No. 20;
2; Mismatches
                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,178
APPLICATION NUMBER: US/07/888,178
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 22,27
REFERENCE/DOCKET NUMBER: CSHL91-02A
TELECOMMUNICATION INFORMATION:
TELEPHORE: 61-861-6240
TELEPHORE: 61-861-6240
INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Made in a lab
US-09-556-877-246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 64.3%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139 DWEVLVLGKLKWDL 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 292 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein PCT-US93-05000-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 GKLVWKIDRLG 18
Lexington
Massachusetts
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                  STATE: M
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CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
CURRENT FILING DATE: 2000-07-20
CURRENT FILING DATE: 2000-07-20
CONTROL SEQ ID NO 247
CONTROL SEC ID NO 247
CONTROL SEQ ID NO 247
CONTROL SEC ID N
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3: /cgn2_6/ptodata/1/pubpaa/PcT_Raw_Pubs_Pepp:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_New_Pubs_Pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

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10: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
                                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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102
1 DWQVLLGKLLWKIDNPGI 18
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Gapop 10.0 , Gapext
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Maximum DB seq length: 200000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                  Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 49, Appl Sequence 216294, Sequence 22731, Sequence 58899, A Sequence 289398, Sequence 125535, Sequence 125535, Sequence 195522, Sequence 6653, Ap Sequence 6631, Ap Sequence 180891, Sequence 18081, Sequence 18081, Sequence 18081, Description 1 US-10-092-750-49 1 US-10-092-750-49 1 US-10-425-115-28939 1 US-10-425-115-28939 2 US-10-425-115-28939 2 US-10-425-115-28939 2 US-10-437-963-119552 2 US-10-437-963-119522 3 US-10-437-963-119522 3 US-10-437-963-13338 5 US-10-424-599-276306 6 US-10-424-599-276306 6 US-10-424-599-276306 6 US-10-424-599-276306 6 US-10-437-963-13338 SUMMARIES 114 117 117 118 118 118 % Query Match Length DB 

; GENERAL INFORMATION:

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1 1 1 6 0 1 1 9 0 4 4	4 4	υ rυ 44. 4	1507 1507 242	0 00 44 4	10-437-963-20079 -10-437-963-20079 -10-094-749-2076	Sequence	
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9.00	24	4.4	1491	91	-10-437-963-155	Sequence	
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44 6 4	4 4 4 4	m m	345 424	Ŋ	US-09-738-626-3866 US-10-424-599-210109	Sequence 3 Sequence	
					ALIGNMENTS		
RESULT 1 US-10-092-750-49 ; Sequence 49, Application US/1009	50-49 49, A	pplicat	ion US	/100	92750		
; Publicati ; GENERAL I	on no NFORM	ATION:	300321	5/AL			
, APPLICAN	T: Ha	mmond,	Philip ulia	3			
, APPLICAN	T: W	right,	Martin	C. ptide	s Interactive with	BCL-X1	
FILE REF	ERENC	E: 5003 CATION	6/0500 NUMBER	02 : US	10/092,750		
; CURRENT	FILIN	G DATE:	2002 MBER: 1	-03-( US 61	07 0/274,526		
, PRIOR FI , NUMBER O	LING F SEQ	DATE: 2 ID NOS	001-03	80-			
; SOFTWARE; SEQ ID NC; LENGTH:	: Fas   49   18	tSEQ fo	r Wind	8 W C	Version 4.0		
TYPE: PR ; ORGANISM US-10-092-75		mo sapi	ens				
	h Si 18;	milarity Conser	100 100 /ative	. 80.	Score 102; DB 14; Pred. No. 1.6e-08; 0; Mismatches 0;	Length 18; Indels 0; Gaps 0;	
ò		OVLLGKI	LWKIDN	PGI	18		
q		DWQVLLGKLLWKID	  TWKIDN	DNPGI	138		
RESULT 2 US-10-424-5	599-21	9-216294					
177	i						

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Sequence 12553.5, Application US/10437963
; Sequence 12553.5, Application US/10437963
; Publication No. US20040123343A1
; Fublication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Bradazuk, Brad
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT PILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 125535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 288398 Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Expanding Sequence Conversed to the Conv
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48.0%; Score 49; DB 17; Length 649;
Best Local Similarity 50.0%; Pred. No. 73;
Matches 8; Conservative 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                               Length 144;
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US-10-425-115-289398
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OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 50.0%; Pred. No. 16;
Matches 8; Conservative 4; Mismatches
                                                                                                                                                                                       ; FEATURE:
; OTHER INFORMATION: Clone ID: 30950545.pep
US-10-767-701-56899
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                                                                                                   TYPE: PRT
ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Zea mays
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NAME/KEY: unsure
         SEQ ID NO 56899
                                                           LENGTH: 144
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21 (53-223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 292731, Application US/10425115
Sequence 292731, Application US/10425115
Sequence 292731, Application No. US20040214272A1
SEQUENCE 1 INFORMATION:
SENSEAL INFORMATION:
SENSEAL INFORMATION:
APPLICANT: Labou, Yihua
APPLICANT: Chou, Yihua
APPLICAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 56899, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REPERBNCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , OTHER INFORMATION: Clone ID: PAT_MRT3847_37342C.1.pep
US-10-424-599-216294
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US-10-425-115-292731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 51.0%; Score 52; DB 15; Best Local Similarity 50.0%; Pred. No. 6.3; Matches 8; Conservative 4; Mismatches 4
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48.0%; Score 49; DB 17;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 8; Conservative 4; Mismatches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Zea mays
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US-10-425-115-292731
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US-10-767-701-56899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53221) B
                                                                                                                                                                                              Gaps
                                                                                                                                                                                              .;
0
                                                                                                                                               Length 446;
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                                                                                                                                                                                            1; Indels
CATION: (1)...(446)
COTHER INFORMATION: unsure at all Xaa locations
FEATURE: PEATURE:
COTHER INFORMATION: Clone ID: PAT_MRT4530_91462C.1.pep
US-10-437-963-195522
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64.3%; Pred. No. 1.1e+02;
tive 1; Mismatches 4;
                                                                                                                                             ; DB 16;
. 1e+02;
                                                                                                                                          Score 47; DB 1
Pred. No. 1e+02
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLECTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UF 09/159162
PRIOR APPLICATION NUMBER: UF 00/159162
PRIOR PELING DATE: 1999-12-16
PRIOR PELING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PALENTIN VET. 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 6653, Application US/09738626; Publication No. US20020197605A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
                                                                                                                                               Query Match
Best Local Similarity 72.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 VLLGKLLWKIDNPG 17
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285 LLGKRLWKLEN 295
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                                                                                                                                                                                                                                             5 LLGKLLWKIDN 15
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; Sequence 195522, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Cao, Yongwei
; APPLICANT: Cao, Yongwei
; APPLICANT: Barbazuk, Brad
; APPLICANT: Barbazuk, Brad
; APPLICANT: Barbazuk, Brad
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Fing
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: US/10/437,963
; CURRENT APPLICATION VUMBER: US/10/437,963
; SEQ ID NOS: 204966
; SEQ ID NOS: 204966
; BENGTH: 446
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 310459, Application US/10425115

Publication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
CURRENT APPLICATION
CURRENT FILING DATE: 2003-04-28
FOUR PROPERTY OF SEQ ID NOS: 369326
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                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                    Query Match
47.1%; Score 48; DB 16; Length 57;
Best Local Similarity 50.0%; Pred. No. 8.6;
Matches 8; Conservative 2; Mismatches 6; Indels
                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT4530_2816C.1.pep
US-10-437-963-125535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 46.6%; Score 47.5; DB 17; Best Local Similarity 30.0%; Pred. No. 90; Matches 9; Conservative 3; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: MRT4577_46196C.1.pep
US-10-425-115-310459
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                                                                                                                                                                                                                                                                          2 WQVLLGKLLWKIDNPG 17
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ORGANISM: Oryza sativa
                          TYPE: PRT
ORGANISM: Oryza sativa
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ORGANISM: Zea mays
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LENGTH: 477
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Sequence 13338 Application US/10437963

Sequence 13338 Application No. US20040123343A1

Sequence 13338 Application No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Shou, Yongwei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Nongeli A.

APPLICANT: Li, Ping

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 30-21(5321)B

CURRENT APPLICATION NOWBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 13338

LENGTH: 215
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Sequence 162659, Application US/10437963

Sequence 162659, Application US/10437963

Sequence 162659, Application No. US20040123343AI

GENERAL INPORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Yongwei

APPLICANT: Wu, Wei

APPLICANT: Wu, Wei

APPLICANT: Barbazuk, Brad

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 162659

TYPE: PRT
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Pred. No. 67;
4; Mismatches 2; Indels
                                                                                                                                                  Length 156;
                                                                                                                                                                                                  Indels
; TYPE: PRT
; ORGANISM: Glycine max
; PEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_124172C.1.pep
US-10-424-599-169611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: PAT_MRT4530_35218C.1.pep
US-10-437-963-133338
                                                                                                                                                Score 46; DB 15;
Pred. No. 49;
                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                  45.1%;
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Best Local Similarity 53.8%;
Matches 7; Conservative
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                                                                                                                                                                     Best Local Similarity 54.5
Matches 6, Conservative
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yougwei Y
TITLE OF INVENTION: Show Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILLE REFERENCE: 38-21 (51223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 276306
LENGTH: 152
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Sequence 169611, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 156
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Best Local Similarity 43.8%; Pred. No. 47;
Matches 7; Conservative 4; Mismatches 5; Indels
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46.1%; Score 47; DB 16; Length 65
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                             ; FEATURE:
; CTHER INFORMATION: Clone ID: PAT_MRT4530_32286C.1.pep
US-10-437-963-130091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: unsure
LOCATION: (1)..(152)
OTHER INFORMATION: unsure at all Xaa locations
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 130091
LENGTH: 652
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                                                                                                                                                                                                                                                                                                                                                                                                            84 DKKILVDMLFWAIDNP 99
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                                                                                                                                                     ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Glycine max
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RESULT 15
US-10-424-599-218482
US-10-424-599-218482
Sequence 218482, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Vande K
APPLICANT: Cao Vangwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53233)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
EIRNGTH: 312.
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Best Local Similarity 46.7%; Pred. No. 99;
Matches 7; Conservative 2; Mismatches 6; Indels
                                                                                                  Score 46; DB 16; Length 305;
Pred. No. 96;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: PAT_MRT3847_39317C.1.pep
US-10-424-599-218482
) ORGANISM: Oryza sativa
FARJURE:
CTHER INFORMATION: Clone ID: PAT_MRT4530_6172C.1.pep
US-10-437-963-162659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Glycine max
ORGANISM: MAME/KEY:
NAME/KEY: unsure
LOCATION: (1)..(312)
PEATURE:
PEATURE:
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Best Local Similarity 53.8%;
Matches 7; Conservative
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70 WKKYTGVLIWKTONP 84
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260 KALLGKWIWKLEN 272
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us-10-092-750-49.rpr

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November 10, 2004, 13:40:53 ; Search time 4.41509 Seconds (without alignments) 392.268 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                        OM protein - protein search, using sw model
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102
1 DWQVLLGKLLWKIDNPGI 18
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Gapop 10.0 , Gapext 0.5
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* Database :

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

SUMMARIES

	Description	othe		hypothetical prote	probable transcrip	transcription regu		cyclin D3 - human	86	ne-	OK cysteine	steine		60K cysteine-rich	60 kDa Cysteine-ri	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	probable lysyl-tRN	membrane protein y	hypothetical prote	mannose-6-phosphat	cell cycle protein	probable transfera	hypothetical prote	GTP-binding protei	hypothetical prote	hypothetical prote	cation efflux syst
SUMMAKIES	Ω	25	81	T29556	F97387	AG2605	H81074	B42822	A35829	A32244	B43584	D71515	C81671	S12602	A86560	T48012	C85823	E90976	C70627	T36123	B64963	T31014	AB2373	D64743	D81868	5	25	T39047	9652	8380
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a	Query Match	50.0		47.1	47.1	47.1	45.1	44.6	44.1		44.1		44.1	44.1	44.1	44.1	43.1	43.1	43.1	٠		43.1	•	ς.		ď.		42.2		41.2
	Score	51	20	48	48	48	46	45.5	45	45	4.5	4.5	45	45	45	45	44	44		44	44	44	43.5	٠	43		43	43	42.5	42
		-	7	m	4	2	9	7	80	6	10																	27		

formate dehydrogen hymothetical profe	probable minor str	acetohydroxy acid	acetolactate synth	fimbrin-like 71 K	beta transducin -	hypothetical prote	two-component hybr	hypothetical prote	cyclin-like protei	cyclin D3 - rat	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote
S18215	T13635	G86062	F91216	JC7170	T40510	A86222	AC2236	A84647	C40035	JC4012	AB1475	T24972	T24970	875753
H 6	1 (1	7	~	~	~	~	7	7	N	7	CI	N	7	N
306	512	548	548	579	736	810	865	1660	237	293	553	639	698	240
41.2	41.2	41.2	41.2	41.2	41.2	41.2	41.2	41.2	40.7	40.7	40.7	40.7	40.7	40.2
4.4	4 4	42	42	42	42	42	42	42	41.5	41.5	41.5	41.5	41.5	41
		_				_	m	39	_	_	~1		_	

## ALIGNMENTS

RESULT 1 T33259 hypothetical protein C24B9.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Bacession: T3329 R;Murray, J;Wohldmann, P.; Langston, Y.; O'Neal, D. Submitted to the EMBL Data Library, May 1998 R;Murray, J;Wohldmann, P.; Langston, Y.; O'Neal, D. R;Mocession: T3329 A;Reference number: Z21310 A;Reference number: Z21310 A;Reference number: Z21310 A;Ression: T3329 A;Residues: 1-309 cMUR> A;Residues: 1-309 cMUR> A;Residues: 1-309 cMUR> A;Residues: L309 cMUR> A;Generics: Strain Bristol N2; clone C24B9 C;Genetics: A;Map position: Z226/1; Z73/1; 298/3 C;Superfamily: Caenorhabditis elegans hypothetical protein C16D9.7
 Query Match       50.0%; Score 51; DB 2; Length 309;         Best Local Similarity 40.0%; Pred: No. 2.2;         Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;         Qy 1 DWQVILGKLIAKIDN 15         Cb 258 EWMIVLAQLIAWIDH 272
 RESULT 2  G86615  G86615  G86615  C, Species: Lactococcus lactis subsp. lactis subsp. lactis (strain IL1403)  C, Species: Lactococcus lactis subsp. lactis C, Species: Lactococcus lactis subsp. lactis C, Accession: G86815  R, Bolotin, A.; Wincker; P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrl Genome Res. 11, 731-753, 2001  A, Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis A, Reference number: A86625; MUID:21235186; PMID:11337471  A, Status: preliminary A, Gross-references: UNIPROT:09CFF1; GB:AE005176; PID:g12724526; PIDN:AAXO5625.1; G8PDB A, Cross-references: UNIPROT: Status IL1403 C, Genetics: A, Genes: yphA
 Query Match 49.0%; Score 50; DB 2; Length 207; Best Local Similarity 61.1%; Pred. No. 2;

Matches

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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell, R. Arginere, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Residues: 1-275 <TET>
A, Cross-references: UNIPROT.Q9JYL8; GB:AE002501; GB:AE002098; NID:g7226755; PIDN:AAF418
A, Experimental source: serogroup B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cyclin D3 - human
NyAleernate names: PRAD1/cyclin D1 proto-oncogene homolog
C;Species: Homo sapiens (man)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 12-Jul-2004
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 12-Jul-2004
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 12-Jul-2004
C;Accession: B44022; I60850
R;Xiong, Y: Menninger, J: Beach, D:; Ward, D.C.
Genomics 13, 575-584, 1992
A;Title: Moleoular cloning and chromosomal mapping of CCND genes encoding human D-type
A;Accession: B42822.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.cross-references: UNIPROT:QBUIQ4; GB:AE008688; PIDN:AAL41261.1; PID:g17738567; GSPDB:
A.Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ritettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Solience 287, 1809-1815, 2000
A,Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A;Reference number: Alloon, Mulb:20175755; PMID:10710307
A,Accession: H81074
A,Accession: H8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phytoene synthase-related protein NVB1521 [imported] - Neisseria meningitidis (strain C;Species: Neisseria meningitidis C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004 C;Accession: H81074
                                                                                                                                                                                                                                                                                             C58.
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                                                                                                                                                                                                                                                           ster, E.W.
A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens
A/Reference number: AB2577; MUID:21608550; PMID:11743193
A/Accession: AG2605
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Pred. No. 12;
2; Mismatches
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0; Mismatches
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A;Map position: circular chromosome
C, Accession: AG2605
P:Wood, D.W.; Setubal, J.C.; Kaul,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.1%;
58.3%;
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DWLIMLKKALWK 275
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Best Local Similarity
Matches 9; Conserv
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Matches 7; Conserv
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Asmolecule type: DNA
AsResidues: 1-290 «KUR»
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A;Residues: 1-292 <XIO>
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20556
R;Gattung, S: Le, T.T.
submitted to the EMBL Data Library, July 1996
A;Description: The sequence of C. elegans cosmid C16D9.
A;Reference number: 220640
A;Accession: T20556
A;Accession: T20556
A;Accession: T20556
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T2054 cGMT>
A;Residues: 1-254 cGMT>
A;Reperimental source: strain Bristol N2; clone C16D9
C;Genetics:
A;Genetics:
A;Genetics: 123/3; 166/3; 213/1; 238/3
C;Superfamily: Caenorhabditis elegans hypothetical protein C16D9.7
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C)Species: Agrobacterium tumefaciens
C)Species: Ob-6ep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C)Accession: F97387
R)Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2332-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
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A,Status: preliminary
A,Status: preliminary
A,Residus: Draliminary
A,Residus: 1-258 «KUR»
A,Cross-references: UNIPROT:Q8UIQ4, GB:AE007869, PIDN:AAK86055.1; FID:g15155128, GSPDB:GCGenetics:
A,Gene: AGR C_407
A,Map position: circular chromosome
C;Superfamily: arabinose operon regulatory protein
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C,Species: Agrobacterium tumefaciens
C,Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
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47.1%; Score 48; DB 2; Length 254;
Best Local Similarity 40.0%; Pred. No. 5.2;
Matches 6; Conservative 7; Mismatches 2; Indels
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                     Indels
                     7;
                     Mismatches
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                                                                                               1 DWQVLLGKLLWKIDNPGI 18
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les 9, Conservative
                     11; Conservative
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ઠ q Query Match Best Local Si Matches 9,

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RESULT 5

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RiAllen, J.E.; Stephens, R.S.
J. Bacteriol. 171, 285-291, 1989
A.Title: Identification by sequence analysis of two-site posttranslational processing c A,Reference number: A32244; MUD:89123030; PMID:2914847
A,Reference number: A32244; MUD:89123030; PMID:2914847
A,Molecule type: DNA
A,Molecule type: DNA
A,Mosesperimental source: Strain L2/434/Bu
A,Experimental sourc
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A;Molecule type: DNA
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Rosidues: 1-46;528-547 <LAM>
A;Cross-references: GB:M35148; GB:M23180; GB:M35161; NID:g144485
A;Cross-references: GB:M35148; GB:M23180; GB:M35161; NID:g144485
A;Cross-reference: GB:M35148; GB:M23180; GB:M35161; NID:g144485
A;Clarke, I.N.; Ward, M.E.; Lambden, P.R.
Gene 71, 307-314, 1988
A;Pitle: Molecular cloning and sequence analysis of a developmentally regulated cystein
A;Reference number: JT0419; MUID:89138006; PMID:3066701
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A; Residuaes: 1-547 < DELS.

A; Cross-references: GB:N23001; NID:g144552; PIDN:AAA23152.1; PID:g144553

A; Experimental source: serovar 2, strain L2/434/Bu

R; Wahlberg, J.; Lundeberg, J.; Hultman, T.; Uhlen, M.

B; Wahlberg, J.; Lundeberg, J.; Hultman, T.; Uhlen, M.

A; Title: General colorimetric method for DNA diagnostics allowing direct

A; Reference number: A36043; MUID:90370827; PMID:2118652
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A;Cross-references: GB:M35148; NID:g144485; PIDN:AAA23119.1; PID:g144487
A;Experimental source: serotype L1
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C;Date: 05-Dec-1998 #sequence revision 05-Dec-1998 #text_change
C;Accession: B43584; S13120; B18979; S24275
R;de la Maza, L.M.; Fielder, T.J.; Carlson, E.J.; Markoff, B.A.;
Infect. Immun. 59, 1196-1201, 1991
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Pred. No. 36;
1; Mismatches 2; Inde
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A;Residues: 294-402 <MAH>
A;Resperimental Source: serotype L2
R;Lambden, P.R.; Everson, J.S.; Ward, M.E.; Clarke, I.N.
Gene B7, 105-112, 1990
A;Title B1, Sulfur-rich proteins of Chlamydia trachomatis:
A;Reference number: JQ0514; MUID:90236284; PMID:2332164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.18;
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159 GKLVWKIDRLG 169
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C; Function:
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          A,Cross-references: UNIPROT:930281, GB:M90814; NID:9180002; PIDN:AAA51927.1; PID:9180003
A,Note: sequence extracted from NCBI backbone (NCBIN:109687, NCBIP:109688)
B;Notcokura, T.; Keyomarsi, K.; Kronenberg, H.M.; Arnold, A.
J. Biol. (Chem. 267, 20412-20415, 1992
A;Title: Cloning and characterization of human cyclin D3, a cDNA closely related in sequal Reference number: A4022; MUD:93018922; PMID:1383201
A;Recence number: A4022; MUD:93018922; PMID:1383201
A;Recence number: A4022; MUD:93018922; PMID:1383201
A;Recence type: mRNA
A;Resperimental source: placenta hackbone (NCBIP:115738)
A;Cross-references: GB:M92287; NID:9181246; PIDN:AA452137.1; PID:9181247
A;Experimental source: placenta hackbone (NCBIP:115738)
B;Inaba, T.; Marsushime, H.; Valentine, M.; Roussel, M.F.; Sherr, C.J.; Look, A.T.
Genomics 13, 565-574, 1992
A;Title: Genomic organization, chromosomal localization, and independent expression of hackeference number: A42821; MUID:92347850; PMID:1386335
A;Accession: 160850
A;Accession: 160850
A;Accession: 160850
A;Accession: GB:M88087; NID:9180014; PIDN:AA51929.1; PID:9180016
C;Genetics:
A;Gene: GB:CCND3
A;Access-references: GB:M88087; NID:33834
A;Access-references: GB:M88087; NID:33834
A;Access-references: GB:M88087; NID:33834
A;Access-references: GB:M88087; NID:33834
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C.Species: Chlamydia trachomatia
C;Daetes: 12-Oct-1989 #sequence revision 27-Jun-1994 #text change 09-Jul-2004
C;Accession: A32244; A43584; Ā36043; A30472; JT0419; S18981; S24277
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64.3%; Pred. No. 15;
:ive 2; Mismatches
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A;Introns: 66/3; 138/3; 122/1
A;Note: introns line may be incomplete
C;Superfamily: cyclin, A/B/D/E type
C;Keywords: cell cycle control
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Matches 7; Conservative
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nes 9; Conserv
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A;Status: not compared with conceptual translation A;Molecule type: DNA
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Best Local Similarity 72.7%;
Matches 8; Conservative .
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Best Local Similarity 72.7%;
Matches 8; Conservative
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166 GKLVWKIDRLG 176
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A;Residues: 1-556 <ARN>
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A; Title: Sequence diversity of the 60-kilodalton protein and of a putative 15-kilodalton A; Reference number: A43584; MUID:91147205; PMID:1997423
A; Reference number: B43584
A; Molecule type: DNA
A; Residues: 1-547 < DEL>A; CACOSS-references: UNIPROT:P23603; EMBL:X54389; NID:940763; PIDN:CAA38259.1; PID:940764
A; Residues: 1-547 < DEL>A; Seperimental source: strain Bour, serotype E
R; Coles, A.M.; Allan, I.; Pearce, J.H.
Nucleic Acids Res. 18, 6713, 1990
A; Title: The nucleotide and derived amino acid sequence of the omp2 gene of Chlamydia tr
A; Reference number: S13120; MUID:91067486; PMID:2251143
A; Reference number: S13120; MUID:91067486; PMID:2251143
A; Residues: 1-32, FF', 33-120, L', 122-131, 'A', 133-457, 'S', 459-547 < COL>
A; Residues: 1-32, FF', 33-120, L', 122-131, 'A', 133-457, 'S', 459-547 < COL>
A; Residues: 1-32, FF', 33-120, L', 122-131, 'A', 133-457, 'S', 459-547 < COL>
A; Residues: 1-32, FF', 33-120, L', 122-131, 'A', 133-457, 'S', 459-547 < COL>
A; Residues: 1-32, FF', 33-120, L', 122-131, 'A', 133-457, 'S', 459-547 < COL>
A; Residues: 1-32, FF', 33-120, L', 122-131, 'A', 133-457, 'S', 459-547 < COL>
A; Residues: 1-32, FF', 33-120, L', 122-131, 'A', 133-457, 'S', 459-547 < COL>
A; Residues: 1-32, FF', 33-120, L', 122-131, 'A', 133-457, 'S', 459-547 < COL>
A; Residues: 1-32, FF', 33-120, L', 122-131, 'A', 133-457, 'S', 459-547 < COL>
A; Residues: 1-32, FF', 33-120, L', 122-131, 'A', 133-457, 'S', 459-547 < COL>
A; Residues: 1-32, FF', 33-120, L', 122-131, 'A', 133-457, 'S', 459-547 < COL>
A; Residues: 1-32, FF', 33-120, L', 122-131, 'A', 133-457, 'S', 459-547 < COL>
A; Residues: 1320, FF', 33-120, L', 122-131, 'A', 133-457, 'S', 459-547 < COL>
A; Residues: 1320, FF', 33-120, L', 122-131, 'A', 133-457, S', 132-1320, TS', 132-132
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R;Stephens, R.S.; Kalman, S; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998

R;Stephens, R.S.; Kalman, S; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Sqience 282, 754-759, 1998

A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachy A;Reference number: A71570; MUID:9900809; PMID:9784136

A;Reference number: A71570; MUID:9900809; PMID:9784136

A;Residues: 1-553 <ARN>
A;Residues: 1-553 <ARN>
A;Resperimental source: serotype D, strain UW-3/Cx

R;de la Maza, L.M.; Fielder, T.J.; Carlson, E.J.; Markoff, B.A.; Peterson, E.M.
Infect. Immun. 59, 1196-1201, 1991

A;Title: Sequence diversity of the 60-kilodalton protein and of a putative 15-kilodalton A;Reference number: A43584; MUID:91147205; PMID:1997423

A;Recession: C43584

A;Recessi
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A; Experimental source: serotype C
R; Watson, NW.; Lambden, P.R.; Ward, M.E.; Clarke, I.N.
R; Watson, NW.; Lambden, P.R.; Ward, M.E.; Clarke, I.N.
FENS Microbiol. Lett. 65, 293-297, 1989
A; Title: Chlamydia trachomatis 60 kDa cysteine rich outer membrane protein: A; Reference number: $11673
A; Molecule type: DNA
A; Residues: 7-553 xAAT>
A; Cross-references: EMBi:X53510; NID:940681; PIDN:CAA37588.1; PID:940683
A; Experimental source: serotype B
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
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Matches
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60K cysteine-rich outer membrane protein precursor [similarity] - Chlamydophila pneumon C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae (cjpate: 30-Sep-1993 #sequence revision 27-Jun-1994 #text_change 09-Jul-2004 C;Accession: 512602; H72651; Aibandawi, P.R.; Clarke, I.N.
Nucleic Acids Res. 18, 5299, 1990
AyTitle: The nuclectide sequence of the 60kDa cysteine rich outer membrane protein of C A;Reference number: 512602; MUID:90384850; PMID:2402463
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A; Residues: 1-556 <WAT>
A; Residues: 1-556 <WAT>
A; Cross-references: UNIPROT:P23700; GB:X53511; NID:G550564; PIDN:CAA37590.1; PID:G55056
A; Cross-references: Uniproc. isolate IOL-207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Chlamydia muridarum, Chlamydia trachomatis Mohn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: C8167,
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis Mohn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUD:20150255; PMID:10684935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;cross-references: UNIPROT:09PJV0, GB:AE002341; GB:AE002160; NID:g7190754; PIDN:AAF395
A;Experimental source: strain Nigg (MoPn)
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R.Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.
Nature Genet. 21, 385-389, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.Experimental source: strain CWL029
R.Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg
A,Note: essential for the structural integrity of the outer envelope of the elementary C,Superfamily: 60K cysteine-rich outer membrane protein C,Keywords: membrane protein; virulence F;1-28/Domain: signal sequence #status predicted <SIG> F;2-46/Domain: propeptide #status predicted <PRO> F;29-46/Domain: propeptide #status predicted <PRO> F;47-553/Product: 60K cysteine-rich outer membrane protein 2 #status predicted <WAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 kDa outer membrane protein TC0727 [imported] - Chlamydia muridarum (strain Nigg)
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Pred. No. 36;
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Pred. No. 36;
1; Mismatches
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Search completed: November 10, 2004, 14:52:18 Job time : 5.41509 secs
A;Introns: 99/1; 605/2
A;Note: T17J13.160
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C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: A86560
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
A;Shirai, Acids Ree. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-556 <REA>
A; Residues: 1-556 <REA>
A; Residues: 1-556 <REA>
A; Cross-references: GB: AE002180; GB: AE002161; NID: G7189117; PIDN: AAF38068.1; PID: G718912
A; Experimental source: strain AR39, HL cells
C; Comment: This protein is associated with the differentiation of reticulate bodies into It may also be an important virulence factor.
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A;Residues: 1-556 <2TO>
A;Cross-references: UNIPROT:P23700; GB:BA000008; NID:g8978928; PIDN:BAA98763.1; GSPDB:GN
A;Experimental source: strain J138
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(S.Species: Arabidopsis thaliana (mouse-ear cress)
(S.Species: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
(S.Accession: T48012
(S.Accession: T48012
(S.Accession: M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Lemcke, K.; Mayer, Submitted to the Protein Sequence Database, February 2000
A;Reference number: Z24482
A;Accession: T48012
A
                                                               A,Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39. A,Reference number: A81500; MUID:20150255; PMID:10684935 A,Accession: A81604
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A;Genetics:
A;Genetics:
C;Genetics:
C;Cyuperfamily: 60K cysteine-rich outer membrane protein
C;Keywords: membrane protein; virulence
C;Keywords: membrane protein; virulence
F;1-22/Domain: signal sequence #status predicted <SIG>F;23-40/Domain: propeptide #status predicted <PRO>F;23-40/Domain: propeptide #status predicted <PRO>F;41-556/Product: 60K cysteine-rich outer membrane protein #status predicted <PAI>F;41-556/Product: 60K cysteine-rich outer membrane protein #status predicted <PAI
F;41-556/Product #status predicted <PAI
F;41-556/Producted 
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Pred. No. 36;
1; Mismatches 2; Indels
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Pred. No. 36;
1; Mismatches 2; Indels
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A;Cross-references: UNIPROT:Q9M1Q4; EMBL:AL138651
A;Experimental source: cultivar Columbia; BAC clone T17J13
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C,Superfamily: 60K cysteine-rich outer membrane protein
Nucleic Acids Res. 28, 1397-1406, 2000
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Best Local Similarity 72.7%;
Matches 8; Conservative
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Best Local Similarity 72.7
Matches 8, Conservative
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168 GKLVWKIDRLG 178
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A;Status: preliminary
A;Molecule type: DNA
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  Length 673;
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 Score 45; DB 2;
Pred. No. 45;
4; Mismatches
                                                                            105 DKKIĽVDMĽFWALDNP 120
 44.1%;
illarity 43.8%;
Conservative
                                                    1 DWQVLLGKLLWKIDNP 16
Query Match
Best Local Similarity
Matches 7; Conserv
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Fri Nov 12 14:55:34 2004
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09tyha schistosoma
09tyha schistosoma
022910 caenorhabdi
07div9 agrobacteri
08uiq4 agrobacteri
08pd2 xanthomonas
08pg16 xanthomonas
085287 leishmania
085289 bacteroides
08n1s8 corynebacte
Caf20884 corynebac
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Q7vt35 bordetella
Q7wfi2 bordetella
Q9d099 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                 076432 caenorhabdi
Q9fnp6 arabidopsis
Q9cff1 lactococcus
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Q9h0j4 homo sapien
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Q6zmy6 homo sapien
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Q7ujp9 rhodopirell
Q9zaw0 chlamydophi
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Q46163 chlamydophi
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                                                            November 10, 2004, 13:38:57; Search time 23.9774 Seconds (without alignments) 431.938 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                              Description
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                    1825181 segs, 575374646 residues
                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
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Q7VT35
Q7WF12
APHC_MOUSE
BAC36101
Q9JYL8
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Maximum Match 100%
Listing first 45 summaries
                                         OM protein - protein search, using sw model
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Q95Z87
Q89ZE9
Q8NLS8
CAF20884
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Q6BFH5
Q46163
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Q6ZMY6
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Q8UIQ4
Q6BW53
Q8PDP2
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Q9TYH3
Q9TYH4
Q22901
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102
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Gapop 10.0 , Gapext 0.5
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2: uniprot_trembl:*
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Q6k9ul oryza sativ Q7nn31 gloeobacter Q7nug anopheles q		Q9ag10 chlamydia p Q61ch5 chlamydia p Q46164 chlamydia p	_	Q986D3 Chlamydla D Q961m3 homo sapien Q6wgp4 chlamydla s
Q6K9U1 Q7NN31 Q7PUQ9	CGD3 HUMAN Q02664 Q9AF82	Q9AG10 Q6LCH5 046164	AABOOS73 QGFNUZ	Q9S6B3 Q96LM3 Q6WGP4
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## ALIGNMENTS

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Caenorhabditis elegans.
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRANIBELISTON N2.
MUTTAY J., Wohldmann P., Langston Y., O'Neal D.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the EMBL/GenBank/DDBJ databases
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InterPro; IPR002651; DUF32.
Pfam; PF01748; DUF32.
Pfam; PF01748; DUF32.

Pfam; PF01748; DUF32.

Mypothetical protein.

SEQUENCE 309 AA; 35650 MW; 7AC2FDIFBIB3C27C CRC64;
                                                                                      076432;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein C24B9.2.
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STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                 PRELIMINARY;
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STRAIN=Bristol N2;
Waterston R.;
Submitted (JAN-2003) t
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Submitted (OCT-2003)
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Submitted (FEB-2004)
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STRAIN-Bristol N2;
Wilson R.;
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Wilson R.;
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                                                                                                                                                                                                                                                             Name=C24B9.2;
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RESULT 1
                                                                 SOW BENEFIT OF THE SECOND SECO
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SEQUENCE FROM N.A. STRAIN=Porto Rico;
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Matches
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MEDLINE=21235186; PubMed=11337471;
BOlotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Structural analysis of Arabidopsis thaliana chromosome 5. II.
Sequence features of the regions of 1,044,062 bp covered by thirteen
physically assigned Pi clones.";
DNA Res. 4:291-300(1997).
EMBL; AB006696; BAB10381.1; -.
GO; GO:0005634; C:nucleus; IEA binding; IEA.
GO; GO:0005270; F:nucleus IEA binding; IEA.
InterPro; IPR007087; Zi C2H2.
InterPro; IPR007087; Zif C2H2.
InterPro; IPR007087; Zif C2H2.
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Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TAXID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-98069011; PubMed-9405937;
Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima N.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
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50.0%; Score 51; DB 2; Length 309; llarity 40.0%; Pred. No. 12; Conservative 7; Mismatches 2; Indels
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; 111222 MW; C824826A49AD7515 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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SMART; SM00451; ZNF_U1; 4.
SMOSITE; PS00028; ZINC_FINGER
SEQUENCE 996 AA; 111222 MW
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258 EWMIVLAQLLWQLDH 272
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Pfam; PF00096; zf-C2H2; 1
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAX-2004 (TrEMBLrel. 26, Last annotation update)
Serine protease SmSPI light chain (Fragment).
Schistosoma manson; (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosoma.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 16, Last sequence update)
Serine protease SmSP1 (Fragment).
Schistosoma mansoni (Blood fluke).
Bukatyota; Merazca; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatidae; Schistosomatidae; Schistosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Submitted (SEP-1998) to the EVBL/GenBank/DDBJ databases.
Submitted (SEP-1998) to the EVBL/GenBank/DDBJ databases.
EVBL; AJO11565; CAA09692.1; -
EVBL; AJO11565; LDHG.
RGSP; P00766; LDHG.
RGSP; P00766; LDHG.
RGSP; P00766; LDHG.
RGSP; P0006235; F:chymotrypsin activity; LEA.
RGS; GO:0006295; F:trypsin activity; LEA.
RGS; GO:0006508; P:proteolylysis and peptidolysis; LEA.
RINTerPro; IPR001314; Peptidase S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.0%; Score 49; DB 2; Length 236; 47.1%; Pred. No. 19;
                                                                                                                                                                                   Length 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Indels
                                                                                                                                                                                                                                        Indels
lactis ssp. lactis IL1403.";
Genome Res. 11:731-753(2001).
EMBL, AE006383; AAX05625.1; -.
CORT, G86815.
CORT, G86815.
SEQUENCE 207 AA; 23410 MW; B4EBE03A872746A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 AA; 26224 MW; FF9C3CDFDBAC2BA4 CRC64;
                                                                                                                                                                                   Score 50; DB 2;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     488 AA.
                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEAM; PF00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM0020; Tryp.SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase, Protease, Serine protease.
NON TER
SEQUENCE 236 AA; 26224 MW; FF9C3C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                           1 DWQVLLGKLLWKIDNPGI 18
                                                                                                                                                                                                                                                                                                                                             74
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WNCIMGKRLCKTRNPGV 221
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                                                                                                                                                                                   Query Match
Best Local Similarity 61.1%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                        sz bweellekspwibavel
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Conservative
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Best Local Similarity
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Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
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QBUIQ4
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    SO DR REPRESENTATION OF THE SO OR REPRESENTATION OF THE SO OF THE 
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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                                                                                                                                                                Cocude C.; SEP-1998) to the EMBL/GenBank/DDBJ databases.
L. SIMILLARITY: Belongs to peptidase family S1.
REMBL; AJO11561; CAA06691.1; -.
REMBL; AJO11561; CAA06691.1; -.
RGJ; GO:0004283; F:chymotrypsin activity; IEA.
GO; GO:0004283; F:chymotrypsin activity; IEA.
RGJ; GO:0004283; F:chymotrypsin activity; IEA.
RGJ; GO:0004289; F:trypsin activity; IEA.
RGJ; GO:0004289; F:trypsin activity; IEA.
RGJ; GO:0006299; F:trypsin activity; IEA.
RILEAPPO; IPR000859; CUB. receptor A.
InterPro; IPR001272; LDL receptor A.
InterPro; IPR001274; Peptidase S1A.
InterPro; IPR00134; Peptidase S1A.
InterPro; IPR00134; Peptidase S1A.
InterPro; IPR00134; Peptidase S1A.
InterPro; IPR00134; Peptidase S1A.
InterPro; IPR00135; Peptidase S1A.
R Pfam; PR00135; LTYPSIN. I.
R SWART; SM00125; LDLA: 1.
R SWART; SM00120; LDLA: 1.
R SWART; SM00120; LDLA: 1.
R RPROSITE; PS501209; LDLRA: 1; I.
R PROSITE; PS00135; TRYPSIN IIS; UNKNOWN. I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 488;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   488 AA; 55029 MW; 29F26792C2014FA6 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
101-ORT-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein C16D9.7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 48.0%; Score 49; DB 2; Local Similarity 47.1%; Pred. No. 41; les 8; Conservative 3; Mismatches
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SEQUENCE FROM N.A.
STRAIN-Bristol N2;
MEDLINE-99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          457 WNCIMGKRLCKTRNPGV 473
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STRAIN=Bristol N2;
Gattung S., Le T.T.;
Submitted (JUL-1996) t.
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NCBI_TaxID=6183;
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SEQUENCE
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SO DE RESERVA DE RESER
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STRAINS-Cereon;

XX MEDLINE-21608551; PubMed=11741194;

XA Goodner B., Gattung S., Miller N., Blanchard M.,

A qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,

A tourollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,

A durollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,

XA Linger M., Doughty D., Scott C., Lappas C., Markelz B.,

R lanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,

XA Cielo C., Slater S.;

T "Genome sequence of the plant pathogen and biotechnology agent

Agrobacterium tumefaciens C58.";

T "Genome sequence of the plant pathogen and biotechnology agent

Agrobacterium tumefaciens C58.";

C = SMILLSTY: Contains 1 HTH arac/xyls-type DNA-binding domain.

EMBL; AE007963; AAR86055 1;

InterPro; IPRO0005; HTHARAC.

PRIMISE: PRO00031; ATAC_binding.

R InterPro; IPRO00065; HTHARAC.

PRIMISE: PRO0005; HTHARAC.

PRIMISE: PRO0005; HTHARAC.

PRIMISE: PRO0005; HTHARAC.

PRIMISE: PRO0005; HTHARAC.
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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OrderediocusNames=AGR C 407;

Agrobacterium tumefaciens (strain CS8 / ATCC 33970).

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.

NCBI_TaxID=176299;
                                                                                                                                                                                                                                                                                                                                                           Length 257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 258;
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                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                        (AUG-2003) to the EMBL/GenBank/DDBJ databases.
                                                        Wilson R.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases
EMBL; UG6858; AAB18286.2; -.
PIX; T29556; T29556.
WormPep; C16D9.7; CE06843.
InterPro; IPR002651; DUF32.
Ffam; PF01748; DUF32; 1.
Hypothetical protein:
SEQUENCE 257 AA; 29578 MW; B2784689FA6664CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3D6D0256E4D65225 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                        Query Match 47.1%; Score 48; DB 2; Best Local Similarity 40.0%; Pred. No. 31; Matches 6; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.1%; Score 48; DB 2; 60.0%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          258 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                              7; Mismatches
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PROSITE; PS0124; HTH_ARAC_FAMILY_2; 1.
DNA-binding; Transcription regulation.
SEQUENCE 258 AA; 29109 MW; 3D600256E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :| ::| :||::|:
198 EWIIVLAQLLWQLDH 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DWOVLLGKLLWKIDN 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 9; Conserv
SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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05-JUL-2004
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host specificities.";
Nature 417:459-463(2002).
BMBL; AE012125; AAM3612.1; -
EMBL; AE012125; AAM3612.1; -
EMBL; AE010136; I'U nucled_hydro.
InterPro; IPR01910; I/U nucled_hydro.
Propom; PF01156; IU nucled_hydro; I.
Propom; PF001736; I'U nucled_hydro; I.
Complete protecome; Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | : | :: |:|| : 315 WHIRLSEIFWEIDNQDV 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 WQVLLGKLLWKIDNPGI 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OrderedLocusNames=XCC0293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 35.3
nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                              Nature 430:35-44(2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleoside hydrolase
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=340;
                                                                                                                                                                                                                                                                                                                                                           STRAIN=CBS767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Matches
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                                                                                                                                                                                                                                                                                                              Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chapman P., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Moster E.W.;

"The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 294:2317-2323(2001).

-!- SIMILARITY: Contains 1 HTH araC/xylS-type DNA-binding domain.

EMBL; AE008996; AAL41261.1; -.

PIR; AG2605; AG2605.

PIR; P97387; F97387.

GO; GO:0005622; C:intracellular; IEA.

GO; GO:0003700; F:transcription factor activity; IEA.

GO; GO:000355; P:regulation of transcription, DNA-dependent; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2004 (TrEMBLrel. 28, Created)
01-0CT-2004 (TrEMBLrel. 28, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
01-0CT-2004 (TrEMBLrel. 28, Cast)
01-0CT-2004 (TrEMBLRel)
01-0CT-2004
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                                                          01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
U-JUNAR-2004 (TrEMBLrel. 26, Last annotation update)
Transcriptional regulator, AraC family.
OrderedLocusNames=Atu0239, (strain CSB / ATCC 33970).
Bachobacterium tumefaciens (strain CSB / ATCC 33970).
Racteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiane, Agrobacterium group; Agrobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 60.0%; Pred. No. 35;
Matches 9; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPRO(3313; AraC_binding.
InterPro; IPRO(39057; Homeodomain_like.
InterPro; IPRO(000557; Homeodomain_like.
InterPro; IPRO(000557; Homeodomain_like.
Pfam; PPO(01655; HTHARAC.
SMART; SMO(3425; HTHARAC.
SMART; SMO(3425; HTHARAC.)
Complete proteone; DNA: Dinding; Transcription regulation.
SEQUENCE 290 AA; 32633 MW; CGF3643FA611B58A CRC64;
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290 AA.
                                          01-JUN-2002 (TrEMBLrel. 21, Created)
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PRT;
                                                                                                                                                                                                                                                                          STRAIN=Dupont;
MEDLINE=21608550; PubMed=11743193;
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PRELIMINARY;
                                                                                                                                                                                                             NCBI_TaxID=176299;
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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GENOLEVURES;
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Q6BW53
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STATIS_ACC 33913

A SILVA A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

A SILVA A.C.R., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

A Alves L.M.C., Go Amaral A.M., Bertollini M.C., Camargo L.E.A.,

A Alves L.M.C., Go Amaral A.M., Dertollini M.C., Camargo L.E.A.,

Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

A Alves L.M.C., Coutinho L.L., Curaino-Santos J.R., El-Dorry H.,

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos E.C., Franco M.C., Gruber A.,

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos E.C., Moon D.H.,

Martins E.C., Machado M.A., Machar A.M. B.N., Martinez-Rossi N.M.,

Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira W.C., Oliveira V.R.,

Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,

Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

Sctubal J.C., Kitajima J.P.,

"Comparison of the genomes of two Xanthomonas pathogens with differing
Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E., Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V., Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C., Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A., Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A., Antrayer F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Karreet A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H., Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O., A. Sellenz S., Potier S., Richard G.F., Streub M.L., Suleau A., Swennene D., Tekaia F., Wasclowski-Louvel M., Westhof E., With B., Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A., Mincker P., Souciet J.L., Scarpelli C., Gaillardin C., Weissenbach J., Wiegenome evolution in yeasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xanthomonas campestris (pv. campestris).
Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales,
Xanthomonadaceae, Xanthomonas.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genoscope;
Submitred (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR382134; CAGB5577.1; -.
SEQUENCE 352 AA; 40083 MW; 40505E557CC2F7EC CRC64;
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Last annotation update)
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01-CCT-2002 (TrEMBLrel. 22, Created)
01-CCT-2002 (TrEMBLrel. 22, Last seq.
01-UTN-2003 (TrEMBLrel. 24, Last ann
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A STRAIN-VPI-5482 / ATCC 29148;

RX MEDLINE=2255088; PubMed=12663928;

RX MEDLINE=2255088; PubMed=12663928;

RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,

RA Chiang H.C., Hooper L.V., Gordon J.I.;

RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";

RI Science 299:2074-2076(2003).

DR EMBL, ABO1945; AAA079533.1;

Complete proteome: Hypothetical protein.

KW Complete proteome: Hypothetical protein.

TO B 2; Length 296;
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
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                                                                                                                                                                                                                                                                                                                                                      Ivens A.C., Murphy L., Quail M., Harris D., Oliver K., Lawson Rajandream M.A., Barrell B.G.; Submitted (UUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL, A1399994; CAC44916.1; -. InterPro; IPR00210.7, ANK. PRINTS; PR01415; ANK.
                                                                                                                      STRAIN=Friedlin;
MEDLINE=98146435; PubMed=9477341;
Ivens A., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
Smith D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Bacteroidetes, Bacteroides (class), Bacteroidales, Bacteroidaceae, Bacteroides.
NCBI_TaxID=818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1864;
                                                                                                                                                                                                                   "A physical map of the Leishmania major Friedlin genome.";
Genome Res. 8:135-145(1998).
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1-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2004 (TrEMBLrel. 29, Last annotation update)
Hypothetical membrane protein (Putative membrane protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.1%; Score 48; DB 2; Le
43.8%; Pred. No. 2.4e+02;
ive 4; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteroides thetaiotaomicron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ilarity 43.8%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
OrderedLocusNames=BT4428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 65...
Tr Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
SEQUENCE 1864 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 7; Conserv
                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                          STRAIN=Friedlin;
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                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Q89ZE9;
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RESIDENCE STRAIN=306 / ATCC 13902 / XV 101;

RESIDENCE STRAIN=306 / ATCC 13902 / XV 101;

RA Gasiva A.C.R., Ferro J.A., Refinach F.C., Farah C.S., Furlan L.R.,

RA Guaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

RA Camarotte G., Cannavan F., Cardozo J.C., Parton M.E.A.

RA Caracelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Fraita J.B., Ferrela A.J.S., Perrelnia M.C., Granargo L.P.,

RA Formighieri E.F., Franco M.C., Greggio C.C., Perro M.I.T.,

RA Formighieri E.F., Franco M.C., Ciruber A., Machina R.P., Lemos E.G.M., Lemos M.V.F.,

RA Formighieri E.C., Machado M.A., Madeira A.M. BN., Martinea R.G., Oliveira M.C., Oliveira W.C.,

RA Martins B.C., Machado M.A., Tamura R.B., Teixeira B.C., Tezza R.I.D.,

RA Pereira H.A., Rossia A., Sana J.A.D., Silve C., de Souza R.F.,

RA Formighieri E.C., Mitalima J.P.;

RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Schubal J.C., Kitalima J.P.;

RA Schubal J.C., Kitalima J.P.;

RA "Comparison of the genomes of two Xanthomonas pathogens with differing RT Most specificities.";

REMEL, ABOIL665; AAA35199:1, --

BR GO; GO:0016787; F:hydrolase activity; IEA.

RA Perolom, PD007736; I/Unucled hydro. 1.

RY Complete Protecome: Hydrolase.

RY Sconnelete Drotecome: Hydrolase.

RY Sconnelete Drotecome: Hydrolase.

RY Sconnelete Drotecome: Hydrolase.

RY Sconnelete Drotecome: Hydrolase.
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                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xanthomonas axonopodis (pv. citri).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                  Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 389;
                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42765 MW; BC69BCDA1BA55D97 CRC64;
              42450 MW; 44684F6D4093D4D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                      01-OcT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Nucleoside hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DBC-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein LT.09.
Name-LT.09; Synonyms-P131.01;
Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.1%; Score 48; DB 2; 63.6%; Pred. No. 47;
                                                                     ..
7
                                                            DB 7
                                                               Score 48; DB 2
Pred. No. 47;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       389 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.68; Pred. wo.
                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                  47.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OrderedLocusNames=XAC0307;
                                        Query Match
Best Local Similarity 63.0
The Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 63.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                              2 WOVLLGKLLWK 12
                                                                                                                                                                                                                               88 WEALYGKLVWK 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  389 AA;
              387 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=92829;
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              SEQUENCE
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095287
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OS Leish
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                                                                                                                                                                                                                                                                                                           "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kalinowski J., Bathe B., Bartels D., Bischoff N., Bott M.,
Burkovski A., Dusch N., Eggeling L., Eikmanns B.J., Gaigalat L.,
Goesmann A., Hartmann M., Huthmacher K., Kraemer R., Linke B.,
MCHARICY A.C., Meyer F., Moeckel B., Pfefferle W., Puehler A.,
Tauch A., Rueckert C., Rupp O., Sahm H., Wendisch V.F., Wiegraebe I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pubmedal19948626;
Ralinowski J., Bathe B., Bartels D., Bischoff N., Bott M.,
Burkovski A., Dusch N., Eggeling L., Eikmanns B.J., Gaigalat L.,
Goesmann A., Hartmann M., Huthmacher K., Kraemer R., Linke B.,
MCHARIDY A.C., Meyer F., Moeckel B., Pfefferle W., Puehler A.,
Tauch A., Rueckert C., Rupp O., Sahm H., Wendisch V.F., Wiegraebe I.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete Corynebacterium glutamicum ATCC 13032 genome sequence and its impact on the production of L-aspartate-derived amino acids and vitamins"; 0. Biotechnol. 104:5-25(2003).

EMBL; APO05283; BAC00253.1; -.

EMBL; APO05283; BAC00253.1; -.

EMBL; EXPROSEMENTES, CARPORDELICAL protein.

GCOMplete protecome; Hypothetical protein.

SEQUENCE 474 AA; 50594 MW; 3810825D5298DDB3 CRC64;
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J. Biotechnol. 104:5-25(2003).
EMBL: BX927156; CAP20884.1; -.
SEQUENCE 474 AA; 50594 MW; 3810825D5298DDB3 CRC64;
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OrderedLocusNames-Cg12859, cg3165;
Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria, Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Corynebacteriaceae, Corynebacterium.
NCBI_TaxID=1718;
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46.1%; Score 47; DB 2; Length 474;
Best Local Similarity 64.3%; Pred. No. 84;
Matches 9; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 46.1%; Score 47; DB 2; Length 474; Local Similarity 64.3%; Pred. No. 84; es 9; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025 Nakagawa;
Nakagawa S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Putative membrane protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
PubMed=12948626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-ATCC 13032 / DSM 20300 / NCIB 10025;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 VLLGSLLWPLAAPG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                          NCBI_TaxID=1718;
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CAF20884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Matches
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Search completed: November 10, 2004, 14:50:08 Job time : 25.9774 secs

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|| : |: | : |: | GATSQSYKQFIEALRERLRGGL 32
TOPOLOGY: linear
MOLECULE TYPE: protein
RESULT 1
US-08-378-761A-71
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ОСООООО ПОООООООООООО
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 71, Appl
Sequence 71, Appl
Sequence 3, Appli
Sequence 9109, Ap
Sequence 862, Appl
Sequence 22829, Appli
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Sequence 26931, A
                                                                                                                                                                                                               November 10, 2004, 13:44:14; Search time 8.05283 Seconds (without alignments) 181.178 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 32617,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/i/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                                GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-08-485-286-71

US-09-489-039A-913

US-09-489-039A-9109

US-09-188-092-862

US-09-188-092-829

US-09-188-092-249

US-09-583-110-3642

US-09-583-110-3642

US-09-583-12-249

US-09-583-12-249

US-09-052-262-8

US-09-052-263-8

US-09-052-263-8

US-09-052-263-8

US-09-052-2931-31694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            478139 segs, 66318000 residues
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Maximum Match 100%
Listing first 45 summaries
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1 GAMEREWAMFLRAASSRIRGGV 22
                                                                                                                                                          - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seg length: 200000000
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395
18
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Maximum DB
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   Sequence 27468, A
Sequence 21750, A
Sequence 21180, A
Sequence 32633, A
Sequence 19788, A
Sequence 2, Appli
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ZIP: 4628

COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IS PPC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SUSTRANT APPLICATION DATA: B0.005/MS-DOS
TLING DATE: 26-JAN-1995
FLING DATE: 26-JAN-1995
FLING DATE: 26-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDRER 7
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 33651
TELECOMMUNICATION INFORMATION:
TELEBHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids
TYPE: ACCURATION OF ACIDS OF ACCURATION ACIDS OF ACIDS O
DB 1;
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41.4%; Score 46; DB 1
Best Local Similarity 36.4%; Pred. No. 7.4;
Matches 8; Conservative 5; Mismatches
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APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PREMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US 60/117,747
FRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 9109
LENGTH: 151
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence 86.2, Application US/09538092
; Sequence 86.2, Application US/09538092
; Patent NO. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; APPLICANT: Glot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same FILE REFREENCE: 1596-54.29
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR PILING DATE: 2000-02-01
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 862
; LEATH. 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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41.4%; Score 46; DB 4; Length 251;
Best Local Similarity 36.4%; Pred. No. 7.5;
Matches 8; Conservative 5; Mismatches 9; Indels
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39.6%; Score 44; DB 4; Length 151;
Best Local Similarity 50.0%; Pred. No. 9.1;
Matches 8; Conservative 3; Mismatches 5; Indels
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LOCATION: (0)...(0)

OTHER INFORMATION: Polypeptide Accession Number P07029

US-09-538-092-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-489-039A-9109; Sequence 9109, Application US/09489039A; Sequence 9109, Application US/09489039A; Patent No. 6610836; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAMEREWAMFLRAASSRIRGGV 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 GATSOSYKOFIEALRERLRGGL 32
                                                                                                         ; EARLIER FILING DATE: 1999-03-30; NUMBER OF SEQ ID NOS: 19; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 3; LENGTH: 251; TYPE: PRT; ORGANISM: Abrus precatorius US-09-538-873-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) OKGANISM: Klebsiella pneumoniae
US-09-489-039A-9109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 REWAMFLRAASSRIRG 20
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US-08-485-286-71

Sequence 71, Application US/08485286

Patent No. 5646026

GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
APPLICANT: WORGAN, ALICE ER

TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF

TITLE OF INVENTION: USING
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDRESS:
ADDRESSEE: ANDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDRESS:
CORRESPONDENCE ADDRESS:
COR
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JOS-09-538-873-3

Sequence 3, Application US/09538873

Sequence 3, Application US/09538873

Sequence 3, Application US/09538873

Sequence 3, Application US/09538873

SETIONAL STATE OF INFORMATION:

APPLICANT: SMALLSHAW, JOAN

APPLICANT: BALUNA, ROXANA G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELICRATING VASCULAR LEAK

TITLE OF INVENTION: SYNDROME (VLS)

FILE REPERENCE: UTSD:603

CURRENT APPLICATION NUMBER: US/09/538,873

CURRENT APPLICATION NUMBER: 60/126,826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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ZIP: 46268

ZIP: 46268

COMPUTER READABLE FORM:

MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,286
FILING DATE:
CLASSIFICATION NUMBER: US/08/485,286
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/485,286
FILING DATE: 26-JAN-1995
ATFORNEY/AGENT INPORMATION:
NAME: BORUCKI, ANDRER: 33651
REFERENCE/DOCKET NUMBER: 38272B
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION OF 71:
SEQUENCE CHRARACTERISTICS:
TWO THE TELECOMMUTICATION OF THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: si
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| PARCHA INCORMATION:
| APPLICANT: Giot, Loic
| APPLICANT: Mansfield, Traci A. |
| TILE OF INVENTION: Protein-Protein Complexes and Method of Using Same
| TILE REFERENCE: 15966-542 |
| CURRENT APPLICATION NUMBER: US/09/538,092 |
| CURRENT PILING DATE: 2000-03-29 |
| PRIOR PILING DATE: 1999-04-01 |
| PRIOR PILING DATE: 2000-02-01 |
| PRIOR FILING DATE: 2000-02-01 |
| PRIOR FILING DATE: 2000-02-01 |
| NUMBER OF SEQ ID NOS: 1387 |
| SOFTWARE: CuraPatSegFormatter Version 0.9 |
| SEQ ID NO 249 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (0)...(0)

; OTHER INFORMATION: Polypeptide Accession Number YER102W

US-09-538-092-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPARE: FastSEQ for Windows Version 2.0
SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,207A
FILING DATE: US/08/858,207A
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
ATTORNEY-AGENT UNPORMATION:
NAME: Gimmi, Edward R
REGISTRALION NUMBER: 38,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 301, Application US/08858207A
Fatent No. 6348328
GENERAL INFORMATION:
APPLICANT: Black, Michael
APPLICANT: Hodgson, John
APPLICANT: Michael
APPLICANT: Nicholas, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328el Compounds
NUMBER OF SEQUENCES: 55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 42; DB 4;
Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 38,891
REPERENCE/DOCKET NUMBER: F50475
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
Sequence 249, Application US/09538092
                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 ERKWA--ARAASAKIESSV 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 EREWAMFLRAASSRIRGGV 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.8%;
52.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature LOCATION: (0)...(0)
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                                                                                                                                                                                                                                                                                                                                                APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ACEUCICA AND THERAPEUTICS
CURRENT PAPLICATION NUMBER: US/09/252,991A
CURRENT PAPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Sequence 2523, Application US/09134000C
| Patent No. 6617156
| GENERAL INFORMATION:
| APPLICANT: Lynn boucette-Stamm et al
| APPLICANT: Lynn boucette-Stamm et al
| TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
| CURRENT APPLICATION NUMBER: US/09/134,000C
| CURRENT PILING DATE: 1998-08-13
| PRIOR APPLICATION NUMBER: US 60/055,778
| PRIOR PILING DATE: 1997-08-15
| SEQ ID NOS: 6812
| SEQ ID NO 5253
| LENGTH: 234
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                      Score 43; DB 4; Length 225; Pred. No. 21; A; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 38.7%; Score 43; DB 4; Length 636; Best Local Similarity 50.0%; Pred. No. 68; Astches 8; Conservative 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
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Pred. No. 27;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 MEREWELFLAPYEQAVSELKVKLRG 35
                                                                                                                                                                                                                                                      US-09-252-991A-22829; Sequence 22829, Application US/09252991A; Patent No. 6551795; GENERAL INFORMATION; APPLICANT: Marc J. Rubenfield et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 MEREWAMFL----RAASS---RIRG 20
                                                                                                                                                ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Enterococcus faecalis US-09-134-000C-5253
                                                                                                                  2 AMEREWAMFLRAASSRIR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||||:|||
557 REWAVFLRRVFQHAHG 572
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                   Query Match
Best Local Similarity 38.9%;
Matches 7; Conservative
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Best Local Similarity 44.0%;
Matches 11; Conservative
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US-09-134-000C-5253
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US-09-538-092-249
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0
Query Match 37.8%; Score 42; DB 4; Length 1464; Best Local Similarity 43.8%; Pred. No. 2.5e+02; Matches 7; Conservative 3; Mismatches 6; Indels
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41.2%; Pred. No. 2.8e+02;
tive 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09052469
Patent No. 6380360
GENERAL INFORMATION:
APPLICANT: Haris et al.
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE 1 GENE
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 23
CORRESPONDENCES: Banner & Witcoff, Ltd.
STREET: One Financial Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk, 3.50 inch
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordberfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,469
FILING DATE: 14-APPLICATION DATA:
APPLICATION NUMBER: 08/422,582
FILING DATE: 14-APPLICATION DATA:
APPLICATION NUMBER: GB 9507766.5
FILING DATE: 13-APPLICATION DATA:
APPLICATION NUMBER: GB 9411900.5
FILING DATE: 14-APPRICATION DATA:
APPLICATION NUMBER: GB 92164/02822
FILING DATE: 23-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9326470.3
FILING DATE: 23-DEC-1994
FILING DATE: 24-DEC-1993
ATTORNEY/AGBNT INNORMATION:
NAME: Williams, Ph.D. Kathleen M.
REGISTRATION NUMBER: 3265/74165
FILING DATE: 24-DEC-1993
ATTORNEY/AGBNT INNORMATION:
TELEPHONE: (617) 345-9111
INPORMATION POR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | | : | : | | | 1188 GAADRQWTRFVRGRPRR 1204
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925 DNHWALFAKAVLDRIR 940
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                                                                                                                      4 EREWAMFLRAASSRIR 19
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Best Local Similarity 41.47
Best Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
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CITY: Boston
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                                                                                                                                                                                                                                                                     RESULT 12
US-09-052-469-2
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US-09-583-110-3642, Application US/09583110

Sequence 3642, Application US/09583110

Patent No. 6699703

GENERAL INFORMATION:

APPLICATION

TITLE OF INVENTION:

TITLE OF INVENTION:

PILE REFERENCE:

PATHOO-07A

CURRENT FILING DATE:

CURRENT PILING DATE:

PRIOR APPLICATION NUMBER: US 60/09583,110

PRIOR FILING DATE:

PRIOR PELICATION NUMBER: US 60/085,131

PRIOR FILING DATE:

PRIOR FILING DATE:
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                                                                                                                                                                                                                                                                                                                         6; Indels
                                                                                                                                                                                                                                                               Ouery Match 37.8%; Score 42; DB 3; I Best Local Similarity 35.3%; Pred. No. 1.1e+02; Matches 6; Conservative 5; Mismatches 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-3642
      INFORMATION FOR SEQ ID NO: 301: SEQUENCE CHARACTERISTICS: LENGTH: 671 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                    |: |::|||
189 EKRWSIFLRPVGEDLKG 205
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                                                                                                          ; TOPOLOGY: linear ; MOLECULE TYPE: No. 6348328e US-08-858-207A-301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 35.33
Matches 6; Conservative
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US-08-658-136-5
Sequence 5, Application US/08658136
Sequence 5, Application US/08658136
Patent No. 6071717
APPLICANT: LANDES, GREGORY MAPPLICANT: LANDES, GREGORY MAPPLICANT: LANDES, GREGORY MAPPLICANT: DACKOWSKI, TIMOTHY CAPPLICANT: DACKOWSKI, WILLIAM APPLICANT: GEMINO, GREGORY
APPLICANT: GEMINO, GREGORY
APPLICANT: GEMINO, GREGORY
APPLICANT: GENING : POLYCYSTIC KIDNEY DISEASE GENE NUMBER OF SUGUENCES: S
ADDRESSEE: GENYME CORPORATION
STREET: ONE MOUNTAIN ROAD
CITY: FRAMINGHAM
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: OTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 37.8%; Score 42; DB 4; Length 161
Best Local Similarity 41.2%; Pred. No. 2.8e+02;
Matches 7; Conservative 3; Mismatches 7; Indels
             COUNTRIES

ZIP: COMPUTER READABLE FORM:
MUDIUM TYPE: Floppy disk, 3.50 inch
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC-DOS/MS-DOS
SOCHWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,262
FILING DATE: COMCURTENTLY herewith
APPLICATION NUMBER: 08/422,882
FILING DATE: 13-APR.1995
PRIOR APPLICATION DATE: 13-APR.1995
PRIOR APPLICATION DATE: 13-APR.1995
PRIOR APPLICATION DATE: 13-APR.1995
PRIOR APPLICATION DATE: 14-UNN.1994
PRIOR APPLICATION DATE: 24-DEC.1994
PRIOR APPLICATION NUMBER: GB 9326470.3
FILING DATE: 23-DEC.1994
PRIOR APPLICATION NUMBER: GB 9326470.3
FILING DATE: 23-DEC.1994
APPLICATION NUMBER: GB 9326470.3
FILING DATE: 33-DEC.1994
APPLICATION NUMBER: GB 9326470.3
FILING DATE: 24-DEC.1993
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Ph.D., Kathleen M.
RECISTRATION NUMBER: 34.360
RECISTRATION NUMBER: 34.360
RECISTRATION NUMBER: 34.360
RECISTRATION NUMBER: 34.360
REFERENCE/DOCKET NUMBER: 3265/74118
TELEPHONE: (617) 345-9110
TELEPHONE: 1614 amino acids

MODELLE APPLICATION ACIDS

SEQUENCE CHARACTERISTICS:
LENGTH: 1614 amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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     COUNTRY:
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             Sequence 2, Application US/08422582

Batent No. 6485960

GENERAL INFORMATION: POLYCYSTIC KIDNEY DISEASE 1 GENE
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE 1 GENE
TITLE OF INVENTION: AND USES THEREOF
CORRESSED Banner & Witcoff, Ltd.
STREET: 75 State Street
CITY: Boston
STATE: Hoston
STATE: Hoston
STATE: Hoston
COMPUTER: EADBABLE FORM:
MEDIUM TYPE: Floppy disk, 3.50 inch
COMPUTER: EADBABLE FORM:
MEDIUM TYPE: Floppy disk, 3.50 inch
COMPUTER: EADBABLE FORM:
MEDIUM TYPE: GENERALISH PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
COMPUTER: BALCATION DATA:
APPLICATION NUMBER: GENERALISH
COMPUTER: APPLICATION DATA:
APPLICATION NUMBER: GENERALISH
FILING DATE: 14-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GENERALISH
FILING DATE: 13-APR-1995
FILING DATE: 13-APR-1995
FILING APPLICATION DATA:
APPLICATION NUMBER: GENERALISH
FILING DATE: 13-APR-1995
FILING APPLICATION DATA:
APPLICATION NUMBER: 3265/53313 (MRC-006cx)
TELECOMMUNICATION NUMBER: 3265/53313 (MRC-006cx)
TELECOMMUNICATION NUMBER: 3265/53313 (MRC-006cx)
TELECOMMUNICATION NUMBER: 3265/53313 (MRC-006cx)
TELECOMMUNICATION NUMBER: 3265/53313 (MRC-006cx)
TELEFRAM: (617) 345-910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09052262

Patent No. 665681

GENERAL INFORMATION:

APPLICANT: Harris et al.

TITLE OF INVENTION: AND USES THEREOF

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSE: Banner & Witcoff, Ltd.

STREET: One Financial Center

CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 1614 amino acids
amino acid
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US-09-052-262-2
US-08-422-582-2
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Gaps

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CPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: GEN4-17.8
FELECOMMONICATION OF SEQ 1D NO: 5:
CELEPHONE: 508-672-5415
FILIPHONE: 508-072-6415
FILIPHONE: GON-07-6415
FILIPHONE: 508-072-6415
FILIPHONE: GON-07-6415
FILIPHONE: 508-072-6415
FILIPHONE: 508-072
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Search completed: November 10, 2004, 14:55:37 Job time : 9.10283 secs

Sequence Sequence

Searched:

Run on:

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RESULT 2
US-10-001-835-218
US-10-001-835-218
' Sequence 218' Application US/10001835
' Publication No. US20020160387A1
' GENERAL INFORMATION:
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Best Local Similarity 100.0%;

Matches 22; Conservative 0
TYPE: PRT
CRGANISM: Homo sapiens
US-10-092-750-50
US-10-092-750-50
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                                                                    November 11, 2004, 01:28:30; Search time 25.4453 Seconds (without alignments) 305.399 Million cell updates/sec
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Sequence
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Sequence
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                                                                                                                                                                                                                                                                                                       Published Applications Asia.

(gnz 6/ptodata1/)pubpaa/USO7 PUBCOMB.pep:*

(gnz 6/ptodata1/)pubpaa/USO6 PUBCOMB.pep:*

(gnz 6/ptodata1/)pubpaa/USO6 PUBCOMB.pep:*

(gnz 6/ptodata1/)pubpaa/USO6 PUBCOMB.pep:*

(gnz 6/ptodata1/)pubpaa/USO7 NBW PUB.pep:*

(gnz 6/ptodata1/)pubpaa/USO8 NEW PUB.pep:*

(gnz 6/ptodata1/)pubpaa/USO8 NEW PUB.pep:*

(gnz 6/ptodata1/)pubpaa/USO8 NEW PUB.pep:*

(gnz 6/ptodata1/)pubpaa/USO8 NEW PUB.pep:*

(gnz 6/ptodata1/)pubpaa/USO8 PUBCOMB.pep:*

(gnz 6/ptodata1/)pubpaa/USO8 PUBCOMB.pep:*
          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-001-835-218
US-10-001-835-218
US-10-1389-566-958
US-10-425-115-224673
US-10-424-599-209333
US-10-424-599-209333
US-10-424-599-209333
US-10-437-963-190381
US-10-437-963-190381
US-10-425-115-3886-37
US-10-425-115-31184
US-10-424-599-263656
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                                                                                                                                                                                   1566620 segs, 353225886 residues
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Maximum Match 100%
Listing first 45 summaries
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1 GAMEREWAMFLRAASSRIRGGV 22
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Match Length DB
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Maximum DB
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Result 8 N

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Sequence 340893, Sequence 32056, A Sequence 52081, A Sequence 227829, Sequence 54127, A Sequence 10620, A Sequence 10620, A Sequence 10620, A Sequence 128120, Sequence 2814, Ap Sequence 28120, Sequence 281309, Sequence 281309, Sequence 179626, Sequence 281309, Sequenc
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Sequence 147013,
Sequence 308921,
Sequence 203172,
Sequence 203172
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196344,
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Sequence
Sequence
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Sequence 50, Application US/10092750

Publication No. US20030032157A1

GENERAL INFORMATION:

APPLICANT: Hammond, Philip W.

APPLICANT: Alpin, Julia

APPLICANT: Wright, Martin C.

TITLE OF INVENTION: Polypeptides Interactive with BCL-X1

TITLE OF INVENTION: Polypeptides US/10/092,750

CURRENT FILING DATE: 2002-03-07

PRIOR FILING DATE: 2001-03-08

NUMBER OF SEQ ID NOS: 253

SEQ ID NO 50

LENTH: 22

LENTH: 22
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6 US-10-425-115-325061

6 US-10-767-701-43701

6 US-10-282-1221-08434

6 US-10-437-963-151611

7 US-10-437-963-151611

7 US-10-437-963-15144835

4 US-10-437-963-1544835

6 US-10-437-963-1544835

6 US-10-437-963-1544835

6 US-10-437-963-154835

6 US-10-437-963-15181

7 US-10-425-115-271829

6 US-10-425-114-6054

5 US-10-425-114-6054

6 US-10-425-115-271829

6 US-10-425-115-190434

7 US-10-425-115-190434

8 US-10-425-115-10620

10S-10-425-115-10620

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10S-10-425-115-10620

10S-10-424-599-179626

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2 US-10-424-599-179626
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Pred. No. 1.3e-10;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
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Sequence 224673, Application US/10425115

Fubilication No. US20040214272A1

Fubilication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Yongwi

APPLICANT: Cao, Yongwi

APPLICANT: Cao, Yongwi

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

TITLE OF INVENTION: UNMER: US/10/425,115

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 224673

LENGTH: 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/FR:
LOCATION: (65)..(65)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature

// LOCATION: (165)...(165)

// OTHER INFORMATION: Xaa can be any naturally occurring amino acid

US-10-389-566-558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (43) .. (44)
OTHER INFORMATION: Xaa can be any naturally occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_13648C.1.pep
CURRENT APPLICATION NUMBER: US/10/389,566
CURRENT FILING DATE: 2003-03-31
PRIOR PELLING DATE: 2003-03-15
PRIOR FILING DATE: 2002-05-15
PRIOR FILING DATE: 2002-06-25
PRIOR FILING DATE: 2002-06-26
NUMBER OF SEQ ID NOS: 2459
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (1)...(1)
OTHER INFORMATION: Xaa
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ORGANISM: Zea mays
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Fublication No. US20040058319A1

GENERAL INFORMATION:
APPLICANT: Salceda, Susana
APPLICANT: Recipon, Herve
APPLICANT: Recipon, Herve
APPLICANT: Cafferkey, Robert
APPLICANT: Liu, Yongming
APPLICANT: Liu, Chenghua
ITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Profuncant Liu, Chenghua
ITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Profuncant Pilling Date: 2001-11-20
CURRENT APPLICATION NUMBER: 06/252,061
PRIOR FILLING DATE: 2000-11-27
PRIOR FILLING DATE: 2000-11-27
PRIOR FILLING DATE: 2000-11-27
SOFTWARE PLICATION NUMBER: 66/253,257
PRIOR FILLING DATE: 2000-11-27
SOFTWARE PATENT PATENT ON 107
LENGTH: 82
    APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
APPLICANT: Recipon, Herve
APPLICANT: Can Yongming
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Pro
CURRENY APPLICATION NUMBER: US/10/001,835
CURRENY FILING DATE: 2001-11-20
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Publication No. US20040025202A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Monsanto Technology, LLC
APPLICANT: Laurie, Cathy C
TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 88.3%; Score 98; DB 13; Length 82
Best Local Similarity 90.9%; Pred. No. 6.2e-08;
Matches 20; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                     PRICR APPLICATION NUMBER: 60/249,997
PRICR FILING DATE: 2001-11-20
PRICR FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: Patentin version 3.1
SEQ ID NO 218
LENGTH: 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Homo sapien US-10-001-835-218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-885-107
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US-10-389-566-958
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APPLICANT: GHETIE, VICTOR F.
APPLICANT: SMALLSHAW, JOAN
APPLICANT: SMALLSHAW, JOAN
APPLICANT: SMALLSHAW, JOAN
APPLICANT: SMALLSHAW, JOAN
TILLE OF INVENTION: POPTEINACEOUS COMPOUNDS
TILLE OF INVENTION: PROTEINACEOUS COMPOUNDS
FILE REFERENCE: UTSD.884US
CURRENT APPLICATION NUMBER: US/10/282,935
CURRENT APPLICATION NUMBER: 09/538,873
PRIOR PILING DATE: 2002-10-29
PRIOR FILING DATE: 2000-03-30
PRIOR FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 23
SOFTWARE PARENTIN VET: 2.1
SEQ ID NO 3
LENGTH: 251
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Pred. No. 42;
5; Mismatches 9;
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Publication No. US20040123343A1
APPLICANT: LA ROSA, Thomas J.
APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAMEREWAMFLRAASSRIRGGV 22
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Best Local Similarity 36.4%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT ; ORGANISM: Abrus precatorius US-10-282-935-3
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; ORGANISM: Abrus precatorius
US-10-440-796-3
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US-10-440-796-3
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Sequence 209333, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwai
TITLE OF INVENTION: Plant Applicant and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 28-21(53223)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
SEQUENCE OF SEQUENCE OF SEQUENCE OF SEGUENCE OF SEQUENCE OF SEQUE
                                                                                                                                                                                                                                                                    and Other Molecules Associated With
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             Sequence 270202. Application US/10424599
; Sequence 270202. Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: La Coa Yongue
; APPLICANT: Cao Yongue
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Assc
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: 12033 B
; CURRENT APPLICATION UNMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 270202
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68.8%; Pred. No. 32;
iive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
42.3%; Score 47; DB 15; Length 92;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 10; Conservative 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: PAT_MRT3847_86010C.1.pep
US-10-424-599-270202
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US-10-424-599-209333
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LOCATION: (1)..(189)
PEATURE INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 AMEVEWKKIKRKAAARREGG 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 AMEREWAMFLRAASSRIRGG 21
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Best Local Similarity 68.8<sup>§</sup>
Matches 11; Conservative
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          US-10-424-599-270202
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US-10-282-935-3
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Sequence 263566, Application US/10424599
Sequence 263566, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRENEUE: 321(3223)B
CURRENT APPLICANTON NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 263656
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US-10-425-115-325061

US-10-425-115-325061

Sequence 325061, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)
FILE REFERENCE: 38-21(53222)
CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEG ID NO 325061

LENGTH: 192
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OTHER INFORMATION: Clone ID: PAT_MRI3847_80100C.1.pep
US-10-424-599-263666
                                                                                                     TYPE: PRT
CROADAISM: Zea mays
CROADAISM: Zea mays
CROADAISM:
PEATURE:
COTHER INFORMATION: Clone ID: WRT4577_65144C.1.pep
US-10-425-115-331184
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; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_59526C.1.pep
US-10-425-115-325061
                                                                                                                                                                                                                                                     Score 45; DB 17;
Pred. No. 41;
3; Mismatches 7,
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 331184
LENGTH: 170
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Best Local Similarity 40.7%;
Matches 11; Conservative
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APPLICANT: Staffa, Alfredo
APPLICANT: Stagnanuel
APPLICANT: Stagnanuel
TITLE OF INVENTION: GENES AND PROTEINS INVOLVED IN THE BIOSYNTHESIS OF ENEDIYNE RING
TITLE OF INVENTION: STRUCTURES
FILE REPERENCE: 3011-30S
CURRENT APPLICATE: 2002-05-21
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin version 3.0
SEO ID NO 3.3
LENGTH: 328
                                                                                               APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBNCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT PILLING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 190381
LENGTH: 434
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Sequence 331184, Application US/10425115

Sequence 331184, Application US/10425115

Sequence 331184, Application US/040214272A1

Sequence 331184, Application US/0425115

GENERAL INFORMATION: Thomas J.

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

TITLE REFERENCE: 38-21(53222)B

CURRENT APPLICATION NUMBER: US/10/425,115
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41.0%; Score 45.5; DB 14; Length 328;
Best Local Similarity 32.4%; Pred. No. 67;
Matches 12; Conservative 5; Mismatches 5; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 41.4%; Score 46; DB 16; Length 434; Best Local Similarity 50.0%; Pred. No. 74; Matches 9; Conservative 2; Mismatches 7; Indels
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US-10-437-963-190381
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; Sequence 37, Application US/10152886
; Publication No. US2030064491A1
; PERREAL INFORMATION:
; APPLICANT: ECOPIA BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            390 VRRMWDSFIRAGGSRIPG 407
  Zhou, Yihua
Cao, Yongwei
Wu, Wei
Buukharov, Andrey A.
Barbazuk, Brad
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-152-886-37
                                APPLICANT:
APPLICANT:
APPLICANT:
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RESULT 15
US-10-767-701-43701
is guence 43701, Application US/10767701
is Sequence 43701, Application US/10767701
is Sequence 43701, Application US/10767701
is Sequence 43701, Devid K.
is Publication No. US20040172684A1
is APPLICANT: Zhou, Yihua
is APPLICANT: Zhou, Yihua
is APPLICANT: Zhou, Yihua
is APPLICANT: Zhou, Yongwei
is APPLICANT: Zhou, Yongwei
is TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
is TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
is TITLE OF INVENTION: NUMBER: US10/767,701
is CURRENT APPLICATION NUMBER: US10/767,701
is CURRENT FILING DATE: 2004-01-29
is NUMBER OF SEQ ID NOS: 63128
is SEQ ID NO 43701
is LENGTH: 207
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                                                     0; Gaps
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Pred. No. 1e+02;
1; Mismatches 4; Indels
Query Match
39.6%; Score 44; DB 17; Length 192;
Best Local Similarity 50.0%; Pred. No. 68;
Matches 8; Conservative 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-C13563_1.pep
US-10-767-701-43701
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                                                                                              5 REWAMFLRAASSRIRG 20
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Best Local Similarity 61.5%;
Matches 8; Conservative
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Copyright (c) 1993 - 2004 Compugen Ltd.
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111
1 GAMEREWAMFLRAASSRIRGGV 22
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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1: Dir1:*
2: Dir2:*
3: Dir3:*
4: Dir4:*
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ription		abrin (clone 7.2)		hypothetical prote	aldolase Atul014 [	hypothetical prote	-dire	hypothetical prote	ρ	heterodeneous ribo	GTP-binding protei	conserved hypothet	maltose ABC transp	conserved hypothet	crumbs protein - f	ribosomal protein	probable transfera	hypothetical prote	cal	memb	probable membrane	hypothetical prote	polycystic kidney	conserved hypothet	hypothetical prote	_	ㅁ	invertase, cell-wa	biotin carboxyl ca
SUMMARIES		841	C39761	TZLSA	G83823	AF2701	G97483	E69473	T15628	E82112	A24016	B69069	AG3170	H72205	H75603	A35672	S45591	A70865	T01923	AF2483	S57149	S64782	T08190	A38971	AE0812	T20057	2228	8221	S25151	5557
	DB	10	N	Н	N	N	N	-	N	~	N	N	~	~	N	7	N	7	7	~	N	~	~	7	N	7	7	0	7	7
	Length	249	251	528	231	266	266	488	1166	154	225	399	657	833	458	2139	200	302	521	541	811	1017	1040	4302	149	330	336	458	605	654
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	Score	4,	46	46		45	45	44	44	43	43	43	43	43	42.5	•	42	42	4.2	42	42	42	42	42	41	41	41	41	41	41
	Result No.		N	m	4	ស	ø	7	60	ወ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	20

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A70652	B75633	T31604	E72730	829158	E87413	E83257	A69290	E95870	A39234	A96609	T45653	T35663	AC0675	832430	532431
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1110	1706	377	229	230	243	285	324	346	371	434	447	485	518	527	528
36.9	36.9	36.5	36.0	36.0	36.0	36.0	36.0	36.0	36.0	36.0	36.0	36.0	36.0	36.0	36.0
	41	40.5	40	40	40	40	40	40	40	40	40	40	40	40	40
41															

## ALIGNMENTS

RESULT 1 C84185 hypothetical protein Vng0250c [imported] - Halobacterium sp. NRC-1 C;Species: Halobacterium sp. NRC-1 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Dec-2002 C;Accession: C84185	R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, i Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jab Jung, K.H.; Alam, M.; Freitas, T. Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000 A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.;	A; Authle: Genome sequence of Halobacterium species NRC-1. A; Title: Genome sequence of Halobacterium species NRC-1. A; Reference number: A84160; MUID:20504483; PMID:11016950 A; Accession: C84185 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-249 <sto> A; Cross-references: GB:AE004437; NID:g10579889; PIDN:AAG18847.1; GSPDB:GN00138 C; Genetics: A; Gene: VNG0250C C; Superfamily: uncharacterized conserved protein</sto>	Query Match 41.4%; Score 46; DB 2; Length 249; Best Local Similarity 63.2%; Pred. No. 5.6; Matches 12; Conservative 2; Mismatches 3; Indels 2; Gaps 1;	Qy 4 EREWAMFLRAASSRIRGGV 22 :	RESULT 2  C39761 abrin (clone 7.2) precursor - Indian licorice (fragment) NyContains: RNA N-glycosidase (EC 3.2.2.22) C;Species: Abrus precatorius (Indian licorice) C;Date: 21-Reb-1992 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004 C;Accession: C39761; 814471 R;Evensen, G.; Mathiesen, A.; Sundan, A. J. Biol. Chem. 266, 6848-6852, 1991 A;Title: Direct molecular cloning and expression of two distinct abrin A-chains. A;Reference number: A39761; MUD:91201329; PMID:2016300 A;Accession: C39761 A;Nolecule type: DNA A;Residues: 1-251 < EVUE A;Residues: 1-251 < EVUE A;Residues: 1-251 < EVUE A;Residues: 1-251 < EVUE A;Residues: Data Library, October 1990 A;Reference number: S14471 A;Rocession: S14471 A;Rolecule type: DNA
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A, Reference number: S/4110; MULD:9700919; FILD:030009.
A, Reference number: S/4110 and S/410
A, Residues: 89-108|154-112 and S/410
A, Residues: 89-108|154-112 and S/4110
A, Residues: 89-108|154-112 and S/411
A, Residues: 100 and S/411
A, Residues: 262-276, X', 278-280;329-348;369-388;399-418 and S/410
A, Residues: 262-276, X', 278-280;329-348;369-388;399-418 and S/410
A, Residues: 262-276, X', 278-280;329-348;369-388;399-418 and S/410
A, Residues: 262-276, X', 278-280;329-348;369-388;399-418 and S/4100
C, Superfamint: Abrin-a is more toxic than ricin. The toxin consists of an A chain, which in C, superfamily: ricin; RNA N-91ycosidase homology
C, Superfamily: rNA N-91ycosidase homology and S/410
F;7-246/Domain: RNA N-91y
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A;Experimental source: strain C-125
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                                                                                                                                               A; Molecule type: protein
A; Residues: 262-297, Y', 299-426, 'L', 428-466, 'P', 468-482, 'L', 484-528 <CHE>
K; Lin, S. H.; Chow, L. P.; Chen, Y. L.; Liaw, Y. C.; Chen, J. K.; Lin, J. Y.
Eur. J. Biochem. 240, 564-569, 1996
A; Title: Probing the domain structure of abrin-a by tryptic digestion.
A; Reference number: S74110; WUID: 97008945; PMID: 8856055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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41.4%; Score 46; DB 1; Length 528;
Best Local Similarity 36.4%; Pred. No. 12;
Matches 8; Conservative 5; Mismatches 9; Indels
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                               A;Title: The complete primary structure of abrin-a B chain.
A;Reference number: S24133; MUID:92371656; PMID:1508674
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47.1%; Pred. No. 7.6;
iive 2; Mismatches 7
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11 GATSQSYKQFIEALRERLRGGL 32
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A;Residues: 1-231 <STO>
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                                                                                                                        A; Accession: S24133
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N; Contains: RRNA N-9Jycosidase (BC 3.2.2.2)

N; Contains: RRNA N-9Jycosidase (BC 3.2.2.2)

C; Species: Abrus precatorius (Indian licorice)

C; Date: 31-Dec-1933 #sequence revision 01-Aug-1997 #text_change 09-Jul-2004

C; Accession: S32429; JT0202; Ā33761; JC1399; S14472; S24133; S74110; S74111

R; Hung C. H.; Lee, M. C.; Lee, T. C.; Lin, J. Y.

J. Mol. Biol. 229, 263-267, 1993

A; Title: Primary structure of three distinct isoabrins determined by cDNA sequencing. CA

A; Reference number: S32429; MUD: 9313798; PMID: 8421313

A; Accession: S33429

A; Status: nucleic acid sequence not shown

A; Molecule type: mRNA

A; Residues: 'E', 2-528 *HUN>

A; Cross-references: UNIPROT: P11140; GB:M98344; NID: 9166294; PIDN: AAA32624.1; PID: 9166295

A; Note: the coding region for the sequence shown is preceded by an ATG codon

A; Note: residues 1-8 were derived from the synthesized primer

R; Funatsu, G; Taquchi, Y; Kamenosono, M: Yanaka, M.

Agric. Biol. Chem. 52, 1095-1097, 1988

A; Title: The complete amino acid sequence of the A-chain of abrin-a, a toxic protein from A; Accession: JT0202
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A;Rolecule type: DNA
A;Residues: 'E',2-251 <EVE>
A;Cross-references: GBX54872
A;Across-references: GBX54872
A;Note: residues 1-8 were derived from the synthesized primer
B;Kimura, M.; Sumizawa, T.; Funatsu, G.
B;Stimura, M.; Sumizawa, T.; Funatsu, G.
A;Kimura, M.; Sumizawa, T.; Funatsu, G.
A;Across-reference number: 37, 166-169, 1993
A;Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, toxic
A;Reference number: JC1398; MUID:93169023; PMID:7763422
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A; Motes the amino-terminal state forms pyrrolidone carboxylic acid; therefore, we last the amino-terminal and a. i. Sundan, A. B; Evensen, G.; Mathiesen, A.; Sundan, A. A; Sundan, A. Biol. Chem. 266, 6848-6852, 1991
A; Title: Direct molecular cloning and expression of two distinct abrin A-chains. A; Reference number: A39761; MUID:91201329; PMID:2016300
A, Residues: 'M',1-251 <EV2>
A; Cross-references: EMBL:X54872; NID:g16088; PIDN:CAA38654.1; PID:g16089
C; Superfamily: ricin; rRNA N-g1ycosidase homology.
C; Superfamily: ricin; rRNA N-g1ycosidase; lectin; toxin
C; Reywords: duplication; g1ycosidase; hydrolase; lectin; toxin
F; 1-251/Product: abrin (clone 7.2) chain A #status predicted <ACH>
F; 7-46/Domain: rRNA N-g1ycosidase homology <ARNO
F; 74,113; 1956,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F; 164,167/Active site: Glu, Arg #status predicted
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A,Rocession: JC1398
A,Roledues: 261-347,77,349-351,74,353-357,7L,359-528 <KIM>
A,Resperimental source: seed
R,Evensen, G.; Mathiesen, A.; Sundan, A.
submitted to the EMBL Data Library, October 1990
A,Description: Direct molecular cloning of two distinct abrin A-chains.
A,Reference number: S14471
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A; Residues: 'ME', 2-251 < EV2>
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Best Local Similarity
---s 8; Conserva
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A; Status: preliminary
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A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae. A;Reference number: A69250; MUD:98049343; PMID:9389475
A;Accession: E69473
A;Accession: E69473
A;Accession: E69473
A;Realducin acid sequence not shown; translation not shown
A;Molecule type: DMA
A;Realducin type: DMA
A;Cross-references: UNIPROT:028484; GB:AE000979; GB:AE000782; NID:92689302; PIDN:AAB894
C;Superfamily: DNA polymerase II small subunit, archaeal type; phosphoesterase core hom C;Keywords: metalloprotein; nucleotidyltransferase
F;228-326/Domain: phosphoesterase core homology <PEC>
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A)Experimental source: serogroup O1; strain N16961; biotype E1 Tor
C;Genetics:
A;Gene: VC2146
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein C25H3.9 - Caenorhabditis elegans
C;Species: Genorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T15628
B;Johnson, D.
Submitted to the EMBL Data Library, June 1995
A;Bestiption: T16 sequence of C. elegans cosmid C25H3.
A;Reference number: Z18379
A;Reference number: Z18379
A;Accession: T1562B
A;Accession: T1668
A;Accession: T1668
A;Accession: T1668
A;Residues: 1-1166 «JOH»
A;Residues: 1-1166 «JOH»
A;Residues: BmBL:U29535; NID:g868251; PID:g868258; PIDN:AAA68787.1; CESP:C25H3.
A;Accession: Strain Bristol N2
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Cispecies: Vibrio cho
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A;Gene: CBSP:C25H3.9
A;Introns: 45/3; 82/3; 129/2; 180/2; 202/1; 215/3; 252/1; 374/3; 544/2; 1028/3; 1108/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 44; DB 1; Length 488;
Pred. No. 23;
4; Mismatches 7; Indels
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243 LEKEWEMFVRWLKGEVGG 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 MEREWAMFLRAASSRIRG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Matches 7; Conserv
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A;Molecule type: DNA
A;Residues: 1-154 <HEI>
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aldolase Atu1014 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Accession: AF2701
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, I erage, G.; Giller, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Ster, E.W.
A;Titler The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Residues: 1-266 <KUR>
A;Residues: 1-266 <KUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable DNA-directed DNA polymerase (EC 2.7.7.7) delta small chain - Archaeoglobus fulg
N;Alternate names: conserved hypothetical protein AF1790
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Accession: E69473
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
G;Accession: Z; Zhou, L.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
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52.4%; Pred. No. 8.7;
tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 45; DB 2
; Pred. No. 8.7;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: circular chromosome
C;Superfamily: 2,4-dihydroxyhept-2-ene-1,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GADVTEFANTLRALSARYKGG 256
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Best Local Similarity 52.4%;
Matches 11; Conservative
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Best Local Similarity 52.4%
Marches 11, Conservative
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C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
B;Accession: AG3170
B;Wood, D;W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell, Farp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT.Q9X2P5; GB:AE001820; GB:AE000512; NID:g4982411; PIDN:AAD368 A;Experimental source: strain MSB8 C;Genetics: A;Gene: TM1836
                                                                                                                                                                                                                                                                        A;Molecule type: DNA'
A;Residues: 1-57 «KUR»
A;Cross-references: UNIPROT:08UKL1; GB:AE008687; PIDN:AAL45781.1; PID:g17743516; GSPDB:(
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            maltose ABC transporter, permease protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: 11-dun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: H72205
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 399, 323-329, 1999
A,Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A,Reference number: A72200; MUID:99287316; PMID:10360571
A,Accession: H72205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C,Accession: H75603
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.,
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A,Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A,Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                      ster, E.W.
A, Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A, Reference number: AB2577, MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C,Species: Deinococcus radiodurans
C,Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 833;
59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.7%; Score 43; DB 2;
ilarity 40.0%; Pred. No. 46;
Conservative 5; Mismatches
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Pred. No.
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nilarity 57.1%;
Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                 A;Genome: plasmid
C;Superfamily: bcsA protein
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Best Local Similarity
Matches 8; Conserv
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Matches 8; Conserv
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A, Status: preliminary
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C;Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 09-Jul-2004
C;Accession: A24016
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ilarity 50.0%; Pred, No. 28;
Conservative 2; Mismatches 6. Thable
             Length 154;
                                                                                                                                                                                                                                        heterogeneous ribonuclear particle protein C - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 225;
                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Indels
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Pred. No. 16;
               2;
             DB :
             Query Match
Best Local Similarity 44.4%; Pred. No. 11;
Matches 8; Conservative 3; Mismatches
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150 GILERNWERLLRKAAS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38.7%;
38.9%;
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                                                                                               3 MEREWAMFLRAASSRIRG
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Best Local Similarity
Matches 7; Conserv
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Matches 8; Conserv
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Gaps

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Indels

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J.D.; Dodson, R.J.; T.; Zalewski, C.; M

AG3170 conserved hypothetical protein Atu5090 [imported] - Agrobacterium tumefaciens (strain CS

RESULT 12

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Gaps

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Indels

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C;Accession: A35672.
R;Tepass, U.; Theres, C.; Knust, E.
R;Tepass, U.; Theres, C.; Knust, E.
A;Title: crumbs encodes an EGF-like protein expressed on apical membranes of Drosophila A;Reference number: A35672, MUID:90263104; PMID:2344615
A;Accession: A35672
A;Accession: A35672
A;Kesidues: preliminary
A;Molecule type: mRNA
A;Residues: 1-2139 <TRPA
A;Accessive ferences: UNIPROT:P10040; GB:M33753
A;Note: the authors translated the codon GGC for residue 1928 as Cys, and TAT for residu
                                                                            A;Residues: 1-458 <WHI>
A;Residues: 1-458 <WHI>
A;Cross-references: UNIPROT:Q9RZ60; GB:AE001862; GB:AE001825; NID:g6460468; PIDN:AAF1224
A;Experimental source: strain R1
C;Genetics: A;Gene: DRA0094
A;Map position: 2
C;Superfamily: Haemophilus influenzae hypothetical protein H11500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                crumbs protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 21-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                     38.3%; Score 42.5; DB 2; Length 458; 50.0%; Pred. No. 39; tive 3; Mismatches 7; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       432 GHADRFWAAALGRRASTRVVGG 453
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F,392-424/Domain: EGF homology <EGF1>
F,691-722/Domain: EGF homology <EGF>
F,767-799/Domain: EGF homology <EGR3>
F,1878-1914/Domain: EGF homology <EGX2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Gene: FlyBase:crb
A,Cross-references: FlyBase:FBgn0000368
C,Keywords: transmembrane protein
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Best Local Similarity 47.1:
Matches 8; Conservative
A;Accession: H75603
A;Status: preliminary
A;Molecule type: DNA
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STRAIT=NRC-1 / ArCC 700922 / JCM 11081;

MEDLINE=20504483; PubMed=11016950;

AM BEDLINE=20504483; PubMed=11016950;

AM STATE=1 S. Vernedy S.P., Mahairas G.G., Berquist B., Pan M.,

Swartzell S., Well T., Hall T., Dan N., Sprogna J.,

Swartzell S., Well D., Hall J., Dan S., Thorsson V., Sbrogna J.,

A schartzell S., Well E., Hough D.W.,

Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,

Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

Rebardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;

R. Genome sequence of Halbacterium species NRC-1.;

Proc. Natl Acad Sci. U.S.A. 97:12176-12181(2000).

BRBL; AE004988; AAG18847.1; -..

RIRE, PROC. Natl Acad Sci. U.S.A. 97:12176-12181(2000).

RIRE, PROC. PROC. SCI. U.S.A. 97:12176-12181(2000).

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Bad07736 oryza sat
028494 archaeoglob
089924 bradyzhisob
081045 phomo sapien
061145 photobacter
cag22525 photobacter
081649 homo sapien
09bia3 caenorhabdi
07x14 oryza sativ
08mjf3 canis famil
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Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
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Pred. No. 34;
2; Mismatches
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Q7XCS3
Q94HY3
Q62GA1
BAD07736
DP2S_ARCFU
Q89P24
Q61WK5
C6LJK5
CAG22525
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Abrin A-chain (Fragment).
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Q6evp5 yersinia ps
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Q8th77 oryza sat
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Q7nnr6
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Copyright (c) 1993 - 2004 Compugen Ltd.
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MEDLINE=94139756; PubMed=8307038;

Chih-Hung H., Lee M.C., Chen J.K., Lin J.Y.;

Chih-Hung and expression of three abrin A-chains and their mutants actived by site-specific mutagenesis in Escherichia coli.";

Lu J. Blochem. 219:83-87(1994).

C. -! CATALYITC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 288 FRAN.

C. SIMILARITY: Belongs to the ribosome-inactivating protein family.

R. SIMILARITY: Belongs to the ribosome-inactivating protein family.

R. SIMILARITY: Phydrolase activity; IEA.

GO; GO:0010598; F: FRAN N-glycosylase activity; IEA.

GO; GO:001748; P: negative regulation of protein biosynthesis; IEA.

R. GO; GO:001748; P: pathogenesis; IEA.

R. Pfam; PF00161; RIP; 1.
                                                                                                                          Chin-Hung H., Lee M.C., Chen J.K., Lin J.Y.;

"Cloning and expression of three abrin A-chains and their mutants
"Cloning and expression of three abrin A-chains and their mutants
Bur. J. Blochem. 219:83-87 (1994).

-! CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
specific adenosine on the 26S TRNA.

-! SIMILARITY: Belongs to the ribosome-inactivating protein family.

EMBL. 75720; CAA54138.1, -.

PERMI: PF00161; RIP. 1

PFam; PF00161; RIP. 1

PROSITS; P800925; SHIGARICIN.

PROSITS; P800275; SHIGARICIN.

PROSITS; P800275; SHIGARICIN.

PROSITS; P8004055; Protein synthesis inhibitor; Toxin.
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01-FBS-1997 (TrEMBLrel. 02, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Abrin A chain B164A/R167L; (Fragment).
Name=pcDNAC-1-E164A/R167L;
Abrus precatorius (Indian licorice) (Crab's eye).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; endicotyledons; core eudicots; rosids; eurosids I; Fabales; Pabaceae; Papilionoideae; Abrese; Abrus.
Abrus precatorius (Indian licorice) (Crab's eye).

Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I; Fabales, Fabaceae, Papilionoideae, Abreae, Abrus.
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Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
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251 AA; 27997 MW; 3B60351839AEFB7E CRC64;
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-I. CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S FRNA.

-I. SIMILARITY: Belongs to the ribosome-inactivating protein family. HSSP; P11140; LABR.
                                                                          Gaps
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Name=pcDNAAc-1-E164A/R167L;
Name=pcDNAAc-1-E164A/R167L;
Abrus preadsorius (Indian licorice) (Crab's eye).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,

Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I; Fabales, Fabaceae, Papilionoideae, Abreae, Abrus.
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GO; GO:0030598; F:RNNA N-glycosylase activity; IEA.
GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
GO; GO:0017148; P:pathogenesis; IEA.
InterPro; IPR001574; RIP.
PFam; PF00161; RIP; 1.
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Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
41.4%; Score 46; DB 2; Length 251; llarity 36.4%; Pred. No. 34; Conservative 5; Mismatches 9; Indels
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Best Local Similarity 36.4%; Pred. No. 34;
Matches 8; Conservative 5; Mismatches 9; Indels
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28040 MW; D57FCB182E0EECC9 CRC64;
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01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Abrin A Chain (E164A) (Fragment).
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252 AA

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Evensen G., Mathiesen A., Sundan A., Submitted (OCT-1990) to the EMBL/GenBank/DDBJ databases.
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MEDLINES-22423060; PubMed=12534463;
Melon K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
Madugu R., Melson W.C., White O., Peterson J.D., Khouri H.M.,
Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
Moazzez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
                                                                                                                                                                                                                                                                                                                                                                                Ricin A-Chain type 73 (Fragment).

Abrus precatorius (Indian licorice) (Crab's eye).

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae, Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      specific adenosine on the 28S rRNA.
-!-SIMILARITY: Belongs to the ribosome-inactivating protein family.
EMBL; X54873; CAA38655.1;
HSSP; P11140; IABR.
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GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR001574; RIP.
Pfam; PF00161; RIP; 1.
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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PROSITE; PS00275; SHIGA_RICIN; 1.
Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252 AA; 28229 MW; 187B8B4E134AECE5 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
OrderedLocusNames=PP3706;
                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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12 GATSOSYKOFIEALRERLRGGL 33
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                                                                                                                                                                                                                                       038761; 096234
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                                                                                                           Chih-Hung H., Lee M.C., Chen J.K., Lin J.Y.;
"Cloning and expression of three abrin A-chains and their mutants derived by site-specific mutagenesis in Escherichia coli.";
Eur. J. Biochem. 219:83-87/11294).
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28s rRNA.
-!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
EMBL. STAF222: CAA54140:1;
-- HSSP; P11140; LABR.
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Submitted (OCT-1990) to the EMBL/GenBank/DDBJ databases.

-!- CATALYTIC ACTIVITY: Endobydrolysis of the N-glycosidic bond at one

specific adenosine on the 28S TRNA.

-!- SIMILARITY: Belongs to the ribosome-inactivating protein family.

EMBL; X54812; CAA38654.1; --

PIR; C39761; C39761.
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Bukaryota, Viridiplantae, Ereptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
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GO; GO:0030598.-F:rRNA N-glycosylase activity; IEA.
GO; GO:0010405; P:negative regulation of protein biosynthesis;
GO; GO:0009405; P:negative regulation of protein biosynthesis;
InterPro; IPR001574; RIP.
PFam; PF00161; RIP; I.
PRINTS; PR00396; SHIGARICIN.
Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
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GO; GO:0030598; F:rRNA N-glycosylase activity; JEA.
GO; GO:0017148; P:negative regulation of protein biosynthesis;
InterPro; JPR00159; RIP.
PFam; PF00161; RIP; 1.
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PROSITE; PS00275; SHIGA_RICIN; 1.
Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
Goldsmith A.D., Lee G.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
Kanilan Neumann G., Kawai J., Kim C., Lam B., Lin J.,
Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,
Davis R.W., Ecker J.R., Theologis A.;
Submitted (Apr. 2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY072162; AAL598411; -.

EMBL, AY05418; AAM2005811; -.
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Bukaryota, Viridiplantee, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudicotyledons, core eudicots, rosids;
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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P11140; P28589;
01-JUL-1989 (Rel. 11, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Abrin-a precursor [Contains: Abrin-a A chain (BC 3.2.2.22) (rRNA N-
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                                                                                                                                                      Query Match
41.4%; Score 46; DB 2; Length 319;
Best Local Similarity 44.4%; Pred. No. 43;
Matches 8; Conservative 5; Mismatches 5; Indels
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                                                                                         Complete proteome; Hypothetical protein.
SEQUENCE 319 AA; 35856 MW; ACA25B56E8D47F39 CRC64;
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metabolically versatile Pseudomonas putida KT2440.";
Environ. Microbiol. 4:799-808(2002).
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
05-VUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein At2g46200.
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                                                                                                                                                                                                                                                     3 MEREWAMFLRAASSRIRG 20
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                     Environ. Microbiol. 4:799-808(;
EMBL; AE016788; AAN69303.1; -.
TIGR; PP3706; -.
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Matches 9; Conservative
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ABRA_ABRPR
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DE Sivosidase), Abrina B chain;

Combigation, Abrina B chain;

Combigation, Abrina B chain;

Combigation, Company and Company
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Streptomyces carzinostaticus subsp. neocarzinostaticus.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=167636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.4%; Score 46; DB 1; Length 528; ilarity 36.4%; Pred. No. 71; Conservative 5; Mismatches 9; Indels
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Last sequence update)
Last annotation update)
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Q83U65
Q83U65
Q1-JUN-2003 (TrEMBLrel. 24, Cr
Q1-JUN-2003 (TrEMBLrel. 24, La
O5-JUL-2004 (TrEMBLrel. 27, La
Hypothetical protein (Unbl.)
Name=unbl.
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Best Local Similarity
Matches 8; Conserv
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SEQUENCE FROM N.A.
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AC 08306
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DT 05-JU
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CO Strep
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Agrobacterium tumefaciens (strain C58 / ATCC 33970)
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Best Local Similarity
                                                           SEQUENCE FROM N.A.
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                                    NCBI_TaxID=176299;
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QBUGM2
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                                                                                          Zazopoulos E., Huang K., Staffa A., Liu W., Bachmann B.O., Nonaka K., Ahlert J., Thorson J.S., Shen B., Farnet C.M.;
"A genomics-guided approach for discovering and expressing cryptic metabolic pathways.";
Nat. Biotechnol. 21.187-190(2003).
EMBL; AY117439; AAM78015.1;
EMBL; AF546157; AAO25901.1;
                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
EMBL; AP001511; BAB05110.1; -. PIR; G83823; G83823.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C-125;
MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
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STRAIN=ATCC 15944;
Liu W., Nonaka K., Nie L., Bae J., Zazopoulos E., Farnet C.M.,
Shen E.;
                                                                                                                                                                                                         Score 45.5; DB 2; Length 328;
Pred. No. 54;
5; Mismatches 5; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
40.5%; Score 45; DB 2; Length 231;
Best Local Similarity 47.1%; Pred. No. 46;
Matches 8; Conservative 2; Mismatches 7; Indels
                                     Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                          Hypothetical protein.
SEQUENCE 328 AA; 35711 MW; 7C096FF3C4BA297E CRC64;
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SEQUENCE 231 AA; 27050 MW; F30860E6ACF83ECC CRC64;
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05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
AGR. C. 1872p.
OrderedLocusNames=AGR_C_1872;
                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                             229 GATEOELALFARQAGEHRWALAQGAAFAAEARVRAGL 265
                                                                                                                                                                                                                                                        1 GAMEREWAMFLR------AASSRIRGGV 22
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                                                                                   MEDLINE=22447897; PubMed=12536216;
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                                                                                                                                                                                                            Query Match
Best Local Similarity 32.4%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                         01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-MAR-2004 (TrEMBLrel. 26, BH1391 protein.
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NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus halodurans.
                                                            SEQUENCE FROM N.A. STRAIN=ATCC 15944;
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Q9KD28
ID Q9KD26
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Q7D052
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Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58.",
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Bacteria; Proteobacteria, Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium. NCBI_TaxID=176299;
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Rhizobiaceae, Rhizobium/Agrobacterium group, Agrobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF03328; HpcH Hpal; 1.
SEQUENCE 266 AA; 27934 MW; D37F0891D97D1599 CRC64;
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Last annotation update)
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EMBL; AE009066; AAL42028.1; -.
PIR; AF2701. AF2701.
PIR; G97483; G783.
HSSP; P23522; 1DXE.
G0; G0:0016228; F:aldolase activity; IEA.
InterPro: IFR055000; HpcH_HpaI.
Pfam; PF03328; HpcH_HpaI.
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01-JUN-2002 (TrEMBirel. 21, Last seq
01-JUN-2003 (TrEMBirel. 24, Last ann
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                                                                                                                                                                                                     MEDLINE=21608551; PubMed=11743194;
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EMBL, AE008032; AAK86824.1; ...
InterPro; IPR005000; HpcH HpaI.
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40.5%; Score 45; DB 2; Length 1423;
Best Local Similarity 36.4%; Pred. No. 2.8e+02;
Matches 8; Conservative 5; Mismatches 9; Indels
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Matches 11; Conservative 3; Mismatches
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                                                                                                                                     236 GADVTEFANTLRALSARYKGG 256
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                                                                           1 GAMEREWAMFIRAASSRIRGG 21
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Search completed: November 10, 2004, 14:50:10 Job time : 31.3057 secs

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Sequence 20982, A
Sequence 3124, Ap
Sequence 26751, A
Sequence 75, Appl
Sequence 75, Appl
Sequence 75, Appl
Sequence 76, Appl
Sequence 21550, A
Sequence 2905, Ap
Sequence 2905, Ap
Sequence 2967, A
Sequence 2967, A
Sequence 2967, A
Sequence 2967, A
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 31788, Appl
Sequence 31789, Appl
Sequence 3189, A
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14100, A
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                                                                  November 10, 2004, 13:44:14; Search time 6.58868 Seconds (without alignments) 181.178 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 46,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
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                                                                                                                                                                                                                                                                                                                      Issued Patents AA:*

(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

// cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
// cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
// cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
// cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
// cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
// cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
// cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-583-110-5300

US-09-252-991A-20982

US-09-134-001C-13124

US-09-134-001C-13124

US-09-134-001C-13124

US-09-134-001C-13124

US-09-056-556-75

US-09-072-596-76

US-09-072-596-76

US-09-072-596-76

US-09-252-991A-21750

US-09-252-991A-21788

US-09-252-991A-31788

US-09-252-991A-3178
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US-09-489-039A-14100
US-08-728-603-19
                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                             478139 seqs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                             - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                              US-10-092-750-63
102
1 RGLWVDRVLEEWGLEPRQ 18
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           Copyright
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                                             OM protein
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Sequence 5300, Application US/09583110

; Sequence 5300, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
    APPLICANT: Lynn Doucette-Stamm et al.
    TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus:
    TITLE OF INVENTION: PROBLEM US/09/583,110
    TITLE OF INVENTION: PROBLEM US/09/583,110
    CURRENT APPLICATION NUMBER: US/09/583,110
    CURRENT APPLICATION NUMBER: US 09/107,433
    PRIOR PILING DATE: 1998-06-30
    PRIOR PILING DATE: 1998-06-30
    PRIOR PILING DATE: 1998-05-12
    PRIOR FILING DATE: 1998-05-12
    PRIOR FILING DATE: 1997-07-02
    NUMBER OF SEQ ID NOS: 5322
    SEQ ID NO 5300
    LENGTH: 277
    LENGTH: 277
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US-09-252-991A-20982
US-09-252-991A-20982
Sequence 20982, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: ARRUGINGA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3
     Sequence 12915, A Sequence 4956, Ap Sequence 27210, Ap Sequence 170, Applisequence 170, Applisequence 6, Applisequence 28, Applisequence 28, Applisequence 28, Applisequence 28, Applisequence 28, Applisequence 11397, Ap Sequence 2717, Ap Sequence 2800, Ap Sequence 2540, Ap Sequence 5540, Applis Sequence 55
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US-09-489-039A-12915
US-09-328-312-4956
US-09-252-991A-27210
US-10-106-275-2
US-08-489-039A-8763
US-08-804-227C-15
US-08-804-227C-16
US-08-804-227C-16
US-09-804-237C-17
US-09-101-609-2
US-09-101-609-2
US-09-134-001C-5271
US-09-134-001C-5271
US-09-134-001C-5271
US-09-489-039A-11632
US-09-489-039A-11632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) ORGANISM: Streptococcus pneumoniae US-09-583-110-5300
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RESULT 5

US-09-252-991A-26751

SQUENCE 26751, Application US/09252991A

SQUENCE 26751, Application US/09252991A

SQUENCE 26751, Application US/09252991A

SECURIEMAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ADSCRIPTION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 26751

LENGTH: 431
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APPLICANT: Reed, Steven G.
APPLICANT: Sheiky, Yasir A.W.
APPLICANT: Sheiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
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Pred. No. 47;
4; Mismatches 2; Indels
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; Sequence 75, Application US/08818112
; Patent No. 6290969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 50.0%;
Matches 6; Conservative
380 VWVSGVIDQWGL 391
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STATE: Washing
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Sequence 3124, Application US/09134001C
Sequence 3124, Application US/09134001C
Sequence 3124, Application US/09134001C
Sequence 3124, Application US/09134001C
SENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BEIDERMIDS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BEIDERMIDS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT PELICAN NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR PILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3124
LENGTH: 297
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
US-09-710-279-1434
US-09-710-279-1434
US-09-710-279-1434
US-09-710-279-1434
US-09-710-279-1439
US-09-710-279-1439
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                                                                                                                                                   Length 245;
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                                                                                                                                                DB 4;
8.6;
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Pred. No. 8.6;
3; Mismatches
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                            TYPE: PRT; CRGANISM: Pseudomonas aeruginosa
US-09-252-991A-20982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                             Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
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165 LDRFIDEYGLNPQQ 178
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50 DRAASEWGLQPQE 62
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Best Local Similarity 50.08
Matches 7; Conservative
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   LENGTH: 245
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TREAT

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PATENT NO. 6320456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Steky, Yasir A.W.
APPLICANT: STEWNENTION COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                         COUNTRY: USA

ZIP: 98104-7092

ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUW TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/056,556

FILING DATE: 07-APR-1998

CLASSIFICATION:
75, Application US/09056556
5, 6350456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 21015
TELECOMUNICATION INFORMATION:
TELEPHONE: (206) 682-6031
INFORMATION FOR JOHN
SEQUENCE CHARACTERISTICS:
LENGTH: 580 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                             Washington
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STRANDEDNESS: si
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US-09-056-556-75
                                                                                                                                                                                                                                                     CITY: Seattle
STATE: Washing
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                                                                                                                                                                                                                                    Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Wheto, Antonia
APPLICANT: Gampos-Wheto, Antonia
APPLICANT: Wedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF ADDRESSER: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
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                                                                                                                                                                                  Query Match

44.1%; Score 45; DB 3; Length 580;
Best Local Similarity 52.9%; Pred. No. 65;
Matches 9; Conservative 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Seattle
STATE: Machington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAKY, DAVIG J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 76, Application US/08818111 Patent No. 6338852 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                             1 RGLWVDRVLEEWGLEPR 17
                                                                                                                                                                                                                                                                                                                      82 RTLGVRRTLSOWNLSPR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 KTLGVRKTLSQWNLSPK 98
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 580 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-818-112-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SS: single
linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-818-111-76
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TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Campos-Neto, Antonia
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPCUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 600 Columbia Center, 701 Fifth Avenue
                                                                                  44.1%; Score 45; DB 3; Length 580; 52.9%; Pred, No. 65;
                                                                                                                                  Indels
                                                                                                          Pred. No. 65;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                         Sequence 76, Application US/09072596; Patent No. 6458366
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                              1 RGLWVDRVLEEWGLEPR 17
                                                                                                                                                                                                             82 RILGVRRILSOWNLSPR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                   Query Match
Best Local Similarity 52.9°
single
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RESULT 8 US-09-056-556-75

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RESULT 11
US-09-212-991A-21750

| Sequence 21750, Application US/09252991A
| Sequence 21750, Application US/09252991A
| Sequence 21750, Application US/09252991A
| Patent No. 6551795
| GENERAL INFORMATION:
| APPLICANT: Marc J. Rubenfield et al.
| APPLICANT: Marc J. Ruchenfield et al.
| APPLICANT: Marc J. Ruchenfield et al.
| TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
| TITLE OF INVENTION: NUMBER: US/09/252,991A
| CURRENT FILING DATE: 1999-00-18
| PRIOR APPLICATION NUMBER: US 60/074,788
| PRIOR APPLICATION NUMBER: US 60/094,190
| PRIOR PILING DATE: 1998-07-27
| NUMBER OF SEQ ID NOS: 33142
| SEQ ID NOS: 33142
| LENGTH: 371
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APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEEC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709_2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR PAPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7634
LENGTH: 398
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43.1%; Score 44; DB 4; Length 398;
Best Local Similarity 50.0%; Pred. No. 61;
Matches 8; Conservative 3; Mismatches 5; Indels
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Pred. No. 57;
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pred. No. 65;
1; Mismatches 7; Indels
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US-09-489-039A-7634
; Sequence 7634, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                       1 RGLWVDRVLEEWGLEPR 17
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                                                                                                                                                                                                            Query Match
Best Local Similarity 52.9%;
Matches 9; Conservative
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208 GLGLDKLLRDWGWE 221
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   LENGTH: 580 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity 50.0
Matches 7; Conservative
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US-09-072-967-75
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TYPE: PRI
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APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
IITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
44.1%; Score 45; DB 4; Length 580;
Best Local Similarity 52.9%; Pred. No. 65;
Matches 9; Conservative 1; Mismatches 7; Indels
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOSTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 16:
SEQUENCE CHRARACTERISTICS:
MANDEL: 580 ID NO: 76:
SEQUENCE CHRARACTERISTICS:
TWO THE TOWN OF T
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/072,967
FILING DATE: ..05-MAY-1998
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STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPAN: (206) 622-4900
TELEPAN: (206) 682-6031
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 75, Application US/09072967
Patent No. 6592877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RGLWVDRVLEEWGLEPR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 580 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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US-09-072-596-76
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US-09-072-967-75
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Gaps

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42.2%; Score 43; DB 4; Length 521; 50.0%; Pred. No. 1.2e+02; tive 2; Mismatches 5; Indels
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; PRIOR FILING DATE: 1999-04-09; NUMBER OF SEQ ID NOS: 8344; SEQ ID NO 5969; LENGTH: 521; TYPE: PRT CORANISM: Proceus mirabilis US-09-543-681A-5969
                                                                                                                                                                                                                                                                                                                 1 RGLWVDRVLEEWGL 14
                                                                                                                                                                                                                                                                                                                                                                      63 RRFWLPMLLAEWGL 76
                                                                                                                                                                                                                                      Best Local Similarity 50.0
Matches 7; Conservative
                                                                                                                                                                                                                Query Match
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                                                                                           Sequence 2905, Application US/09540236

Patent No. 6673910

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
FILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERRICE: 2709-2005-001
CURRENT FILING DATE: 2000-04-04

NUMBER OF SEQ ID NOS: 3840

SEQ ID NO 2905
LENGTH: 544
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US-09-543-681A-5969
Sequence 5969, Application US/09543681A
Patent No. 605709
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/543, 681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
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43.1%; Score 44; DB 4; Length 544;
Best Local Similarity 26.1%; Pred. No. 86;
Matches 6; Conservative 8; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 42.2%; Score 43; DB 3; Length 59; Best Local Similarity 57.1%; Pred. No. 11; Matches 8; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/08840767B
; Sequence 14, Application US/08840767B
; Patent No. 6255464;
GENERAL INCORMATION:
APPLICANT: Vogelstein, Bert
APPLICANT: Rigalins, Gragory J.
APPLICANT: Rigalins, Gragory J.
APPLICANT: Rigalingam, Sam
TITLE OF INVENTION: MAD-Related Genes in the Human
FILE OF INVENTION: MAD-Related Genes in the Human
FILE OF INVENTION: MAD-Related Genes in the Human
FILE OF INVENTION: NAMBER: US/08/840,767B
CURRENT APPLICATION NAMBER: 60/015,823
FEARLIER FILING DATE: 1995-04-18
NUMBER OF ESQ.ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1:|:||
262 GIWGEKIMQAWNQFPAGKWGVEP 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GLWVDRVLE-----EWGLEP 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 WVDRVLEEWGLEPR 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: M.catarrhalis
US-09-540-236-2905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
; ORGANISM: C. elegans
US-08-840-767-14
                                               RESULT 13
US-09-540-236-2905
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                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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Sequence 77243, A Sequence 83, App Sequence 86, App Sequence 76, App Sequence 76, App Sequence 50840, App Sequence 176611, Sequence 176611, Sequence 176611, Sequence 228961, App Sequence 228981, App Sequence 652, App Sequence 652, App Sequence 652, App Sequence 922, App Sequence 922,

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Minimum DB s Maximum DB s

Database :

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US-10-092-750-63

Sequence 63, Application US/10092750

Sequence 63, Application US/10092750

Bublication No. US2030032157A1

GENERAL INFORMATION:

APPLICANT: Hammond, Philip W.

APPLICANT: Alpin, Julia

TITLE OF INVENTION: Polypeptides Interactive with BCL-XI

FILE REFREENCE: 50036/050002

CURRENT APPLICATION NUMBER: US/10/092,750

CURRENT FILING DATE: 2002-03-07

PRIOR PLILING DATE: 2001-03-08

PRIOR PLILING DATE: 2001-03-08

NUMBER OF SEQ ID NOS: 253

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 63

LENGTH: BR

TYPE: PRI

5 US-10-424-599-267456

5 US-10-369-267453

4 US-10-369-493-1093

4 US-10-369-493-1093

4 US-10-369-493-1093

4 US-10-084-8843-75

2 US-09-855-604-886

5 US-10-437-963-114917

5 US-10-425-114-45557

5 US-10-425-114-45557

5 US-10-425-114-45257

5 US-10-425-114-70225

6 US-10-425-114-70225

7 US-10-425-114-70225

8 US-10-425-114-70225

9 US-10-425-116-203-678

9 US-10-425-116-203-678

9 US-10-369-493-6778

9 US-10-425-110-286-265

9 US-10-286-266-28

9 US-10-286-266-28

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9 US-10-286-266-28

9 US-10-425-115-286735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-425-114-43310
US-10-425-114-64659
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US-10-425-115-244728
US-10-625-115-24728
Sequence 244728, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RGLWVDRVLEEWGLEPRQ 18

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Sequence 144728,
Sequence 104754,
Sequence 147954,
Sequence 115, App
Sequence 2330, App
Sequence 2765, Ap
Sequence 3765, Ap
                                                                                                                                                                  November 11, 2004, 01:28:30 ; Search time 20.8189 Seconds (without alignments) 305.399 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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4 US-10-15-244728

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6 US-10-437-963-147954

6 US-10-767-701-34655

6 US-10-094-749-233

4 US-10-094-749-233

4 US-10-094-749-235

5 US-10-108-260A-3255

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Maximum Match 100%
Listing first 45 summaries
                                                                                                                       - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1 RGLWVDRVLEEWGLEPRQ 18
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21/53221/B

CURRENT APPLICATION NUMBER: US/10/437,963

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 147954

LENGTH: 582

TYPE: PPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 34655, Application US/10767701

Publication No. US20040172664A1

Publication No. US20040172664A1

Publication No. US20040172664A1

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua,

APPLICANT: Covalic, David K.

APPLICANT: Covalic, David K.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 34655

LENGTH: 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 50.0%; Score 51; DB 16; Length 582; Best Local Similarity 53.3%; Pred. No. 63; Matches 8; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 46.7%; Pred. No. 27;
Matches 7; Conservative 5; Mismatches 3; Indels
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US-10-767-701-34655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ), OTHER INFORMATION: Clone ID: PAT_MRT4530_48433C.1.pep
US-10-437-963-147954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(174)
OTHER__RINFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 WFDRMITEFGIEPTE 134
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ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-767-701-34655
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us-10-C

APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Unucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPRENCE: 38-21(53222)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 244728
LENGTH: 198
TYPE: C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 52; DB 17; Length 198;
Pred, No. 16;
6; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: MRT4577_154781C.1.pep US-10-425-115-244728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (1)..(198)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SQUENCE 10429, Application US/10156761
| Publication No. US20030119018A1
| GENERAL INPORMATION:
| APPLICANT: INEDA, HARUO
| APPLICANT: INFIRAMA, UNN
| APPLICANT: ISHIKAWA, UNN
| APPLICANT: SHIRA, TADAYOSHI
| APPLICANT: SHIRA, TADAYOSHI
| APPLICANT: SHIRA, TADAYOSHI
| APPLICANT: HATYOR! WASAHIRA
| TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
| FILE REFERENCE: 249-262
| CURRENT PLING DATE: 2002-05-29
| CURRENT FILING DATE: 2001-05-30
| PRIOR PRILING DATE: 2001-06-30
| PRICE APPLICATION NUMBER: US DESCRIPTION NUMBER: US DESCRIPTION DATE: 2001-06-30
| PRICE APPLICATION NUMBER: US DESCRIPTION DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-437-963-147954; Sequence 147954; Application US/10437963; Publication No. US20040123343A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-10429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         662 GVALFRLLEEWGVRPR 677
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Best Local Similarity 46.7%;
Matches 7; Conservative t
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76 WFDRMIKEFGIEPAE 90
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NAME/KEY: unsure
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US-10-156-761-10429
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APPLICANT: La Rosa, Thomas J.

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Sequence 5676, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:
APPLICANT: Gao, Yongwei
APPLICANT: Glamar, Barry S.
APPLICANT: Glamar, Barry S.
APPLICANT: Glamar, Barry S.
APPLICANT: Glamar, Barry S.
TILLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TILLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TILLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TILLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TILLE OF INVENTION: UNMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR PILING DATE: 2003-02-28
PRIOR PILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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45.1%; Score 46; DB 14; Length 306;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 3; Mismatches 1; Indels
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44.6%; Score 45.5; DB 9;
Best Local Similarity 69.2%; Pred. No. 63;
Matches 9; Conservative 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: unsure

1 LOCATION: (1)..(306)

2 OTHER INFORMATION: unsure at all Xaa locations

US-10-3869-493-9676
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FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR PLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Desulfitobacterium hafniense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5765, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) ORGANISM: Corynebacterium glutamicum
US-09-738-626-5765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||| :||| :|||
180 RGLWDYIDRVRQEYG 194
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ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RGLW--VDRVLEEWG 13
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APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: IKEDA AKIHIRO
APPLICANT: IKEDA MASATO
APPLICANT: OZAKI, AKIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSI
APPLICANT: ANDO, SEIKO
                                                        US-10-369-493-9676
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Pred. No. 49;
4; Mismatches 4; Indels
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Best Local Similarity 54.5%; Pred. No. 59;
Matches 12; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: HIO, YURI
APPLICANT: OTSUCKA, KAORU
APPLICANT: OTSUCKA, KAORU
APPLICANT: TRIE, KRICHI
APPLICANT: TRRE, RYCTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NACHIKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: NAGAHARI, KENUI
APPLICANT: NAGAHARI, KENUI
APPLICANT: NAGAHARI, KENUI
APPLICANT: NAGHARI, KENUI
APPLICANT: NAGHARI
APPLICAN
FILE OF INVENTION: Proteins
FILE REFERENCE: PWC/P21129WO
CURRENT APPLICATION NUMBER: US/09/769,787
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: GB 9816337.1
PRIOR PLLING DATE: 1998-03-27
PRIOR PLLING DATE: 1998-03-19
NUMBER OF SEQ ID NOS: 388
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 115
LENGTH: 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2330, Application US/10094749
Publication No. US20030219741A1
GENERAL INPORMATION:
APPLICANT: ISCGAI, TRKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TESUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISONO, YUUKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/550,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PATENTIN VOY: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RGLWVDRVLE----EWGLEPRQ 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 46.7%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 WVDRVLEEWGLEPRO 18
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54 WVPRLLQEWKPRPQE 68
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US-10-094-749-2330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JANA
TSONO, IC
YURI
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Gaps

Indels

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Query Match
44.6%; Score 45.5; DB 15;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 12; Conservative 0; Mismatches 1;
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OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 267456, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLWLSRWFTYVMMYWGLHP 34
                                                                                                                                                                                                                                                                                                                           48 RGLWVIRKVLEESEWG 63
                                                                                                                                                                                                                                                                                1 RGLWVDR-VLE--EWG
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3256
LENGTH: 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Glycine max
PEATURE:
NAME/KEY:
LOCATION: (1)...(49)
                                                                                                 TYPE: PRT ORGANISM: Homo sapiens
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US-10-424-599-267456
                                                                                                                                               US-10-108-260A-3256
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                                                                                                                                                 RESULT 10
US-10-100-260A-3255

// Sequence 3255, Application US/10108260A

// Publication No. US20040005560A1

// CENBRAL INFORMATION:

// APPLICANT: HELLY RESEARCH INSTITUTE

// TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA

// TITLE OF INVENTION: No. US20040005560A1e1

// CURRENT APPLICATION NUMBER: US/10/108,260A

// CURRENT PILING DATE: 2002-03-27

// NUMBER OF SEQ ID NOS: 5458

// SOFTWARE: PatentIn Ver. 2.1

// SEQ ID NO 3255

// LENGTH: 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 12.130, Application US/10002631C
; Publication No. US20030157486A1
; GENERAL INFORMATION:
   APPLICANT: Grathon M.
; APPLICANT: Muserics. Matthew
; TITLE OF INVENTION: BURTHODS: TO IDENTIFY SIGNAL SEQUENCES
; TITLE OF INVENTION NUMBER: US/10/002,631C
CURRENT APPLICATION NUMBER: US/10/002,631C
CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: G0/330,309
; NUMBER OF SEQ ID NOS: 324
; SOF ID NO 130
; SEQ ID NO 130
; LENGTH: 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

Query Match

Best Local Similarity 75.0%; Pred. No. 1.1e+02;

Matches 12; Conservative 0; Mismatches 1; Indels
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US-101-108-260A-3256
US-101-108-260A-3256, Application US/10108260A
Sequence 3256, Application US/20108260A
Publication No. US20040005560A1
GENERAL INFORMATION
TITLE OF INVENTION: No. US20040005560A1e1 full length CDNA
TITLE OF INVENTION: No. US20040005560A1e1 full length CDNA
CURRENT APPLICATION WHERE: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
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Pred. No. 1.2e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RGLWVDR-VLE--EWG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 RGLWVIRKVLEESEWG 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 64.3%;
Matches 9; Conservative
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                                                            || |:|:|| |||
75 VDTVIEQWG-EPR 86
                                      5 VDRVLEEWGLEPR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT; ORGANISM: Homo sapiens
US-10-108-260A-3255
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US-10-002-631C-130
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US-10-002-631C-130
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US-10-424-599-148079

US-10-424-599-148079

Sequence 148079, Application US/10424599

Publication No. US20040031072A1

Publication No. US20040031072A1

APPLICANT: La Rosa Thomas J

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5322)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 148079

LENGTH: 49
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: APOLICANT: A Constant of the con
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                                                                                                                                       Gaps
Length 177;
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Best Local Similarity 47.4%; Pred. No. 39;
Matches 9; Conservative 2; Mismatches 4; Indels
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US-10-424-599-148079
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APPLICANT: Vanamoto, Robert
APPLICANT: Vanamoto, Robert
APPLICANT: Yanamoto, Robert
APPLICANT: Your Carr, Grand
APPLICANT: Xu,'H.
ITILE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT PAPLICATION NUMBER: 06/191,078
PRIOR PELICATION NUMBER: 06/206,848
PRIOR APPLICATION NUMBER: 66/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-66
PRIOR FILING DATE: 2000-05-66
PRIOR FILING DATE: 2000-05-66
PRIOR PELICATION NUMBER: 60/230,335
PRIOR PELICATION NUMBER: 60/230,347
PRIOR PELICATION NUMBER: 60/25,625
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR PELICATION NUMBER: 60/25,625
PRIOR PELICATION NUMBER: 60/25,625
PRIOR PELICATION NUMBER: 60/25,636
PRIOR PELICATION NUMBER: 60/25,931
PRIOR PELICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2001-02-09
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                                                                                                                                                                                                   2;
                                                                                                               Score 45; DB 15; Length 131;
Pred. No. 1e+02;
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Pred. No. 2.3e+02;
3; Mismatches 4; Indels
                                                                                                                                                                                               4; Indels
; OTHER INFORMATION: Clone ID: PAT_MRT3847_83536C.1.pep
US-10-424-599-267456
                                                                                                                                                                                               Mismatches
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Publication No. US20040029129A1
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                                                                                                           Query Match
Best Local Similarity 47.1%; Pr
Matches 8; Conservative 3;
                                                                                                                                                                                                                                                                       3 LWVD -- RVLEEWGLEPR 17
                                                                                                                                                                                                                                                                                                                   19 LWSDPEDIVDNWGLSPR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Wang, Liangsu
APPLICANT: Wallone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Yawick, John
APPLICANT: Yamamoto, Robert
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Best Local Similarity 45.09
Matches 9; Conservative
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Search completed: November 11, 2004, 02:43:19
Job time : 21.8689 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 10, 2004, 13:40:53 ; Search time 4.41509 Seconds (without alignments) 392.268 Million cell updates/sec

Title: US-10-092-750-63
Perfect score: 102
Sequence: 1 RGLWVDRVLEEWGLEPRQ 18

Sequence: 1 RGLWVDRVLEEWGLEPRQ 18
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR 79:\*
1: Dir1:\*
2: Dir2:\*
3: Dir3:\*
4: Dir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		de				
Result No.	Score	Query Match	Length	DB	ID	Description
1 1 1 1				1		
п	54		1677	N	834	P-glycoprotein E -
7	51		1724	~1	83	P-glycoprotein - S
m	20	σ.	288	N	G72634	hypothetical prote
4	49	48.0	277	Н	B95072	phosphoesterase-re
Ŋ	4,0		277	Н	-	phosphoesterase-re
9	47.5	46.6	192	7	0	_
7	47		338	~	10	hypothetical prote
œ	46	45.1	244	~		hetical
σ	45	44.1	97	~	~	c
	45	44.1	199	~	~	hypothetical prote
11	45	44.1	290	~1	~	conserved hypothet
	45	44.1	390	-	-	probable hexosyltr
13	45	44.1	437	~	B75067	hypothetical prote
	4.5	44.1	1043	N	~	Ę
	44.5	43.6	303	N		otein ph
	44	43.1	97	N	0	hypothetical prote
	44	43.1	245	~	_	Д
	44	43.1	245	N	D95334	b IS
19	44	43.1	265	N	D82566	GumM protein XF236
	44	43.1	310	N	G83248	probable permease
	44	٠	1308	Ŋ	T05178	al
	43.5	42.6	989	~	T15795	hypothetical prote
	43	42.2	220	0	F84565	meo
	43	٠	305	0	255	
	43	42.2	305	N	255	ein
	43	•	372	~	4485	-4
	43	•	395	~	F82695	덖
	43	42.2	418	~	5501	CEM-1 protein - Ca
	43	42.2	451	N	364	probable tartrate

hypothetical prote	glucosyltransferas	56K serine protein	probable selenium-	probable beta-gala	helicase related p	hypothetical prote	probable MFS trans	hypothetical prote	hypothetical prote	lipoprotein B - Ha	core antigen - gro	homeodomain protei	two-component resp	histidinol-phospha	hypothetical prote
G72205	T40396	PRBEII	D84549	T04269	AC1065	D71543	H83556	T20797	B84152	E64087	NKVLS	H85433	AH1815	A35397	E86634
7	~	Н	~	N	N	N	N	N	N	Н	Н	7	7	~	7
473	206	518	715	729	1249	298	438	97	162	192	217	217	224	361	389
42.2	42.2	42.2	42.2	42.2	42.2	41.7	41.7	41.2	41.2	41.2	41.2	41.2	41.2	41.2	41.2
43	43	43	43	43	43	42.5	42.5	42	42	42	42	42	42	42	42
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

	KESODT. I	
	T18344	
	P-glycoprotein E - Leishmania tropica	
	C;Species: Leishmania tropica	
	C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004	re 09-Jul-2004
-	C;Accession: T18344	
	R;Lafuente, E.; Castanys, S.; Gamarro, F.	
_	submitted to the EMBL Data Library, April 1996	
_	A;Reference number: Z18880	
_	A; Accession: T18344	
_	A;Status: preliminary; translated from GB/EMBL/DDBJ	
	A; Molecule type: DNA	
	A; Residues: 1-1677 < LAF>	
	A; Cross-references: UNIPROT: 000805; EMBL: U55381; NID: 91916605; PID: 91916606; PIDN: AABS1	PID:91916606; PIDN:AABS1
	C, Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology	binding cassette homology
_	Query Match 52.9%; Score 54; DB 2; Length 1677;	
	; Mismatches 6; Indels	0; Gaps 0;
	OW 1 RGIMVDRVLBBMGLBP 16	
	Db 45 RSLWAQRVSDLWGTEP 60	

T18343

PGP/Coprotein - Sauroleishmania tarentolae
C;Species: Sauroleishmania tarentolae
C;Species: Sauroleishmania tarentolae
C;Species: Sauroleishmania tarentolae
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004
C;Accession: T18343
R;Legare, D: Hettema, E.; Ouellette, M.
Mol. Biochem. Parasitol. 68, 81-91, 1994
A;Title: The P-glycoprotein-related gene family in Leishmania.
A;Reference number: Z18879; MUID:95198776; PMID:7891750
A;Accession: T18343
A;Scatus: preliminary; translated from GB/EMBL/DDBJ
A;Status: DNA
A;Molecule type: DNA
A;Residues: 1-1724 <LEG>A;Accession: UNIPROT:Q25425; EMBL:L29485; NID:9460312; PID:9460313; PIDN:AAA6555; C;Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology

Query Match 50.0%; Score 51; DB 2; Length 1724; Best Local Similarity 57.1%; Pred. No. 27; Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Db 47 LWKQRVIDLWGAEP 60

3 LWVDRVLEEWGLEP 16

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RESULT 3

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Gaps 4.

```
C.Accession: 823603
R.Fernandez-Moreno, M.A.; Martin-Triana, A.J.; Martinez, E.; Niemi, J.; Kieser, H.M.; H.G. Bacteriol. 174, 2958-2967, 1992
A.Title: abaA, a new pleiotropic regulatory locus for antibiotic production in Streptom A.Reference number: 823601; MUID:92234955; PMID:1569025
A.Recession: 823601
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-192 < FER-A.Residues: 1-192 < FER-A.C. MIPROT:053897; EMBL:X60316; NID:946793; PIDN:CAA42866.1; PID:95816
            A;Accession: H97939
A;Molecule type: DNA
A;Residues: 1-277 <KUR>
A;Residues: 1-277 <KUR>
C;Coment: Although this sequence has motifs characteristic of a variety of phosphoester C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-338 <STO>
A; Residues: 1-338 <STO>
A; Residues: 1-338 <STO>
A; Experimental source: Strain C-125
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CjAccession: B83861
R;Takami, H; Nakasone, K; Takaki, Y; Maeno, G; Sasaki, R; Masui, N; Fuji, F; Hir:
Nucleic Acids Res. 28, 4317-4331, 2000
N;Ticleic Acids Res. 28, 4317-4331, 2000
A;Reference mumber: A83650; MUID:20512582; PMID:11058132
A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Streptomyces coelicolor
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein BH1690 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                              A)Gene: spr0544
C;Superfamily: phosphoesterase, MJ0912 type; phosphoesterase core homology
F;4-67/Domain: phosphoesterase core homology <PEC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 277;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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A; Reference number: A97872; MUID: 21429245; PMID: 11544234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46.1%; Score 47; DB 2; 77.8%; Pred. No. 20; iive 1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 47.5; DB Pred. No. 9.3; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

80.0%; Score 49; DB 18est Local Similarity 54.5%; Pred. No. 8.1;
Matches 12; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein A - Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RGLWVDRVLE----EWGLEPRQ 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 RGNWDDRVLEALDGQYGLEDPQ 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158 RGLCIVDALAEEWGWTPR 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RGLW-VDRVLEEWGLEPR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 11; Conserva
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les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Start codon: GTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prosphoesterase-related protein SP0619 [similarity] - Streptococcus pneumoniae (strain T C;Species: Streptococcus pneumoniae C;Species: O: Junyan, L.A.; Male; O: Salzberg, S.L.; Lewis, M.R.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey E.K.; Holt, T.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Molecule type: DNA
A;Residues: 1-277 < kUR>
A;Molecule type: DNA
A;Residues: 1-277 < kUR>
A;Comsertences: GB:AE005672; PIDN:AAK74771.1; PID:914972095; GSPDB:GN00164; TIGR:SP4
A;Experimental Source: strain TIGR4
C;Comment: Although this sequence has motifs characteristic of a variety of phosphoester
C;Genetics:
A;Genetics:
A;Genetics: Spod19
                                                                    Cipecacies: Aeropyrum pernix
Cipecacies: Aeropyrum pernix
Cipate: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
Cipate: 21, 11, 1999
And Residus: A. 3. Funahashi, T.; Tanaka, T.; Kudoh, Y.; Janazaki, J.; Runahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Runahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Rittle: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A; Reference number: A72450; MUID:99310339; PMID:10382966
A; Accession: G72634
A; Accession: G72634
A; And A; An
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H97939
H97939
H97939
H97939
H97939
Explosesterase-related protein spr0544 [similarity] - Streptococcus pneumoniae (strain c)Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 15-Sep-2003
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 15-Sep-2003
R;Hoskins, Jal.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M.; Winkler, M.E. M.; Winkler, M.E. M.; Winkler, M.E. M.; Winkler, M.E. John Hallido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ï
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                            pothetical protein APE1534 - Aeropyrum pernix (strain K1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 54.5%; Pred. No. 8.1;
Matches 12; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 50; D
Pred. No. 6;
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151 RGLGSDRVVAEWWLDSR 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49.0%;
ilarity 58.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
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Ubscasses Wibrio cholerae

C;Species: Wibrio cholerae

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C;Cocession: D82233

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.

Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers,

Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers,

Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Residues: DNA

A;Molecule type: DNA

A;Molecule type: DNA

A;Residues: 1-290 «HEI>

A;Cocession: DS233

A;Cocession: DS233

A;Cocession: D82233

A;Co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable hexosyltransferase (EC 2.4.1.-) MJ1607 - Methanococcus jannaschii
Nycleanie hexosyltransferase (EC 2.4.1.-) MJ1607 - Methanococcus jannaschii
Nycleanie ammes: probable lipopolysaccharide N-acetylglucosaminyltransferase rfbU
C;Species: Methanococcus jannaschii
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Ju1-2004
C;Accession: F64500
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
R;Bult, C.J.; Worzbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese,
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese,
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese,
A;Authors: preliminary mucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-390 <BULD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q59002; GB:U67601; GB:L77117; NID:g2826439; PIDN:AAB99629.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
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44.1%; Score 45; DB 1; Length 390;
Best Local Similarity 37.5%; Pred. No. 45;
Matches 9; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 290;
                                                              Length 199;
                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Map position: FOR1581714-1582886
C;Superfamily: probable hexosyltransferase ytxN
C;Keywords: glycosyltransferase; hexosyltransferase
                                                                  2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
                                                           Score 45; DB 2
Pred. No. 23;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 45; DB Pred. No. 33; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Map position: 1
C,Superfamily: hypothetical protein H11400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---VDRVLEEWG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 RNLWLPAGVEPVWKDWGLSP 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RGLW----VDRVLEEWGLEP 16
                                                              44.1%;
ilarity 61.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 45.0%;
Matches 9; Conservative
                                                                                                                                                                                                          3 LWVDRVLEEWGLE 15
                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 8; Conserv
N
A; Map position:
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                                                                                                                                 Cipacte: 11-Un-1999 #squence_revision 11-Uun-1999 #text_change 21-Uul-2000
Cipactesion: T08480
Cipactesion: T08480
Cipacted, P.B.; Shah, D.S.; Macartney, D.; Kostelidou, K.; Thomas, C.M.
Plasmid 36, 95-111, 1996
A; Title: Conservation of the genetic switch between replication and transfer genes of In A; Reference number: 216434; MUID:97118926; PMID:8954881
A; Reference mumber: 216434; MUID:97118926; PMID:8954881
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: 1-97 < THO.
A; Cross-references: EMBL:U67194; NID:g1572520; PIDN:AAC64424.1; PID:g1572529
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C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Species: O3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T40079
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Volckaert, G.
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Volckaert, G.
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Volckaert, G.
A;Reference number: Z21904
A;Reference number: Z21904
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-199 < LYN>
A;Residues: 1-199 < LYN>
A;Residues: 1-199 < LYN>
A;Experimental source: strain 972h-; cosmid c29A3
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Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 97;
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Larity 53.8%; Pred. No. 11;
Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 46; DB 2;
Pred. No. 20;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kleF protein - Enterobacter aerogenes plasmid R751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ?9
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RGLYGDALIEALGLKPKE 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RGLWVDRVLEEWGLEPRQ 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 44.4%;
Matches 8; Conservative 6
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C, Genetics:
A, Gene: SPDB: SPBC29A3.08
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11
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A,Gene: kleF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
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43.6%; Score 44.5; .DB 2; Length 303; S6.2%; Pred. No. 42; tive 1; Mismatches 5; Indels 1
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Job time : 5.41509 secs
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Best Local Similarity 56.21
Matches 9; Conservative
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AB0370
multidrug efflux protein [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Species: Versinia pestis
C;Species: Versinia pestis
C;Species: O2-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB0370
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
Geno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB00370
A;Accession: AB0370
A;Accession: AB0370
A;Molecule type: DNA
A;Residues: 1-1043 -KUR>
A;Cross-references: UNIPROT:Q8ZCE8; GB:AL590842; PIDN:CAC922285.1; PID:g15980996; GSPDB:GCGGenetics:
C;Genetics: YPO3043
C;Superfamily: acriflavin resistance protein
                                                                                                                                                                                                                         C.Species: Pyrococcus abyes:
C.Species: Pyrococcus abyes:
C.Jate: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C.Jate: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C.Jaceslain: B78067
R.Janonywous, Genoscope
submitted to the EMBL Data Library, July 1999
A.Pescription: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stry
A.Reference number: A75001
A.Accession: B78067
A.Accession: B78067
A.Accession: B78067
A.Accession: B78067
A.Accession: Colored abyes: B78067
A.Accession: B7
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A45640
phosphotocein phosphatase (EC 3.1.3.16) 2A catalytic chain - Trypanosoma brucei
C;Species: Trypanosoma brucei
C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2004
C;Accession: A45640
R;Erondu, N. E.; Donelson, J. E.
Nol. Biochem. Parasitol. 49, 303-314, 1991
A;Title: Characterization of trypanosome protein phosphatase 1 and 2A catalytic subunits
A;Reference number: A45640; MUID:92131067; PMID:1663579
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                                                                                                                                                                                                        hypothetical protein PAB1355 - Pyrococcus abyssi (strain Orsay)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 45; DB 2; Length 437;
Pred. No. 51; 3; Indels
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84.1%; Score 45; DB 2; Length 104

Best Local Similarity 57.1%; Pred. No. 1.3e+02;

Matches 8; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
        328 GIWVYPKNPDSIAWGVDRVLSDWG 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
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Similarity 61.5%;
8, Conservative
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WVPRVIEDISLEP 43
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
                                                                                                                     RESULT 13
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072kg3 thermus the Aas80683 thermus the 00805 leishmania 082y05 pyrobaculum 093hi8 streptomyce 083qq1 pseudomonas 07exy6 oryza sati 025425 leishmania 029bbs aeropyrum p 07mm50 vibrio vuln 094bs vibrio vuln 094bs streptococc 024qq streptococc 02760 streptococc 02760 streptococc 02760 streptococc 07602 streptococc 07602 streptococc 07602 streptococc 07605 pseudomonas cae9225 pseudomonas cae9225 pseudomonas 061e13 pichia mem 061e13 pichia mem 061e13 pichia mem 061e13 pichia memculu 080x17 mus musculu 080x17 musulu 080x17 mu
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                      sw model
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AAS80683
0,082K05
0,037H18
0,037H18
0,054Z05
0,72KX6
0,054Z05
0,07KK5
0,07KK5
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Q7CN48
Q9WBJ8
Q706MS
CAE92925
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Q6H188
Q6H193
Q8OXL7
Q8BLU5
Q9UVA0
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102
1 RGLWVDRVLEEWGLEPRQ 18
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Match Length DB
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Perfect score:
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Q53897 streptomyce Q6qhq9 alcaligenes Aas49425 alcaligen Q9kc84 bacillus ha Q8k187 rhizobium e Q8a7a2 bacteroides Q6qq13 calocera Q7z1m4 trypanosoma Q6ps15 chlamydomon Aas57092 calocera Q7z1m4 trypanosoma Q6ps15 chlamydomon Aas92601 chlamydom Q9ymv3 lymantria d Q8xs64 ralstonia s Q8u467 pyrobaculum	ALIGNMENTS  SULT 1  2KQ3  Q72KQ3  Q72KQ3  Q72KQ3  Q72KQ3  Q72KQ3  C Q72KQ3  D ERELIMINARY, PRT; 241 AA.  Q72KQ3  C Q72KQ3  C Q72KQ3  D STEMBLE-1. 27, Created)  C S-JUL-2004 (TrEMBLE-1. 27, Last sequence update)  C S-JUL-2004 (TrEMBLE-1. 27, Last sequence update)  C S-JUL-2004 (TrEMBLE-1. 27, Last sequence update)  D S-JUL-2004 (TrEMBLE-1. 27, Last annotation update)  D S-JUL-2004 (TrEMBLE-1. 27, Last sequence update)  S STORE CALL AND A. Last Sequence of the range of ATP-binding protein livG.  NAME-1ivG; OrderedLocusNames=TYCO335;  Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039).  Bacteria; Deinococcus-Thermus; Deinococci; Thermaceae;  NCBI_TAXID-262724;  [1]  ROBE TAXID-262724;  [1]  ROBE TAXID-262724;  [2]  ROBE TAXID-262724;  [3]  ROBE TAXID-262724;  [4]  ROBE TAXID-262724;  ROBE	.276994D CRC64; DB 2; Length 241; .5; .es 3; Indels 0; Gaps 0;	PRT; 241 AA.  Created) Last sequence update) Last annotation update) ransport ATP-binding protein livG. n HB27 / ATCC BAA-163 / DSM 7039).
Q53897 Q6QHQ9 AAS49425 Q9KC84 Q9KC84 Q8RA2 Q6AJD3 AAS57792 Q7ZIM4 Q6PSL5 AAS92001 Q9YWW3 Q8XSC4	PRT; 241  Created) Last sequence Last sequence Last annotat: ansport ATP-1 HB27 / ATCC 18; Deinococc. 18; Deinococc. 18; Cottscl extreme therr (2004).	%; 549D15A222 Score 55; D Pred. No. 4. 0; Mismatche	PRT; 241 Created) Last sequence Last annotat. ransport ATP-1
6.6 6.1 6.1 173 6.1 173 2 6.1 338 2 6.1 391 2 6.1 631 2 6.1 631 631 631 631 631 631 631 631 631 63	ALIGNMENTS  7. 1  93  972KQ3	E 241 AA; 26385 MV Similarity 78.6%; 11; Conservative 4 WVDRVLEEWGLEPR 17 9 WVDRVLELTGLAPR 132	r; . 27, . 27, cid t
20.00.00.00.00.00.00.00.00.00.00.00.00.0	UI 1  072KQ3  072KQ3  072KQ3  072KQ3  05-JUL-2004 (TYEMB 05-JUL-2004 (TYEMB 05-JUL-2004 (TYEMB 05-JUL-2004 (TYEMB 05-JUL-2004 (TYEMB MANALELING; Ordered Thermus. thermophil Bacteria; Deinococ Thermus. hermophil Bacteria; Deinococ Thermophil Bacteria; Deinococ July Rank HP., Krame Wither Genome sequen Thermophilus." Jacobi C., Starkuv Kramk HP., Krame Wither Genome sequen Thermophilus." Jacobi C., Starkuv	SEQUENCE 24 Query Match Best Local Simil Matches 11; C 4 WVDR	RESULT 2 AAS80683 ID AAS80683 AC AAS80683, DT 14-APR-2004 (TEEMBLEE) DT 11-MAY-2004 (TEEMBLEE) DT 11-MAY-2004 (TEEMBLEE) DT 11-MAY-COO4 (TEEMBLEE) DT 11-MAY-COO4 (TEEMBLEE) DT 11-MAY-COO4 (TEEMBLEE) DT 11-MAY-COO35. OS Thermus thermophilus (
	225 225 225 225 225 225 225 225 225 225	SQ Si Quer Best Matcl	RESU AASS 1D AC AC DT DT GN GN

627 AA

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"Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum.",
Proc. Natl. Acad. Sci. U.S.A. 99:984-989 (2002).
EMBL; ABC09798; AAL63191.1; -.
GO; GO:0003824; F:catalytic activity; IEA.
InterPro; IPR00379; Ser estrs.
InterPro; IPR011042; TolB_C.
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=INAZ / AICC 51768 / DSM 7523;
MEDLINE=21664377; PubMed=11792869;
Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                         Archaea; Crenarchaeota; Thermoprotei; Thermoproteales; Thermoproteaceae; Pyrobaculum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 627 AA; 69906 MW; D115B4D625AF09DF CRC64;
                                                                                                             Q8ZYO5;
01-MRR-2002 (TrEMBLrel. 20, Created)
01-MRR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Acylamino-acid-releasing enzyme, conjectural.
OrderedLocusNames=PAE1002;
                                                                                          PRT;
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45 RSLWAORVSDLWGTEP
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Best Local Similarity 64.7.
Best Local 11, Conservative
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Q93HI8
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Lafuerte E., Castanys S., Gamarro F.;

Ly SIMILARITY: Belongs to the BMBL/GenBank/DDBJ databases.

L. SIMILARITY: Belongs to the ABC transporter family.

EMBL; 118344; 718344.

Rol Go.00016021; Cintegral to membrane; IEA.

Rol Go.000016021; Cintegral to membrane; IEA.

Rol Go.00001060; F:ATP-binding; IEA.

Rol Fami, PRO00064; ABC membrane; IEA.

Rol Fami, PRO00064; ABC membrane; IEA.

Rol Fami, PRO00064; ABC membrane; IEA.
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NCBI_TaxID=5666;
Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
                                                                                                             Henne A., Brueggemann H., Raasch C., Wiezer A., Hartsch T., Liesegang H., Johann A., Lienard T., Goll O., Martinez-Arias R., Jacobi C., Starkuviene V., Schlenczeck S., Dencker S., Huber R., Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.; "The genome sequence of the extreme thermophile Thermus
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                                                                                                                                                                                                                                                                                                                           53.9%; Score 55; DB 2; Length 241; 78.6%; Pred. No. 4.5; tive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                            Nat. Biotechnol. 22:547-553(2004).
EMBL. AE017302; AAS80683.1; -.
ATP-binding. 241 AA; 26385 MW; 549D15A22276994D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-UUL-1997 (TrEMBLrel. 04, Created)
01-UUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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PROSITE; PS00211; ABC_TRANSPORTER 1; UNKNOWN_1.
PROSITE; PS50893; ABC_TRANSPORTER_2; 2.
PROSITE; PS500852; RIBOSOWAL S2 1; UNKNOWN_1.
PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
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Best Local Similarity
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Leishmania tropica.
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                      Thermus.
NCBI_TaxID=262724;
                                                                          SEQUENCE FROM N.A.
PubMed=15064768;
                                                                                                                                                                                                                thermophilus."
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ATP-binding
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                                                                                                                 Gaps
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MEDLINE21477423; PubMed=11572948;
MEDLINES.2147743.; Ishlikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces
avermitiis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces avermitilis.
Bacteria, Actinobacteridae, Actinomycetales, Streptomycineae, Streptomyces.
NCBI_TaxID=33903,
51.0%; Score 52; DB 2; Length 627; 64.7%; Pred. No. 34; 2; Indels iive 0; Mismatches 2; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DCT-2004 (TrEMBLrel. 28, Last annotation update)
Modular polyketide synthase.
Name=olmA4; OrderedLocusNames=SAV2892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     metabolites.";
Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
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MEDLINE=22608306; PubMed=12692562;
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1 RGLWVDRVLEEWGLEP 16

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Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae, Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Sasaki T., Matsumoto T., Katayose Y.;
Sasaki T., Matsumoto T., Katayose Y.;
Submitred (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP006049; BAD10739.1;
InterPro; IPR002685; PPR.
InterPro; IPR008940; Prenyl_trans.
Pfam; PP01535; PPR; 7.
TIGRROUTS; PPR; 5.
SEQUENCE 512 AA; 55624 MW; 7B13DC1C3B5FB4D6 CRC64;
                                                                                                                                                              05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
55-UUL-3004 (TreMBLrel. 27, Last annotation update)
Name=OSJNBa0016N23.128;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 GRWYHATLRRWGVEP 191
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46 DRVATEWGLQPQE 58
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les 8; Conservative
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                                                                                   RESULT
Q7EXY6
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Pseudomonadaceae; Pseudomonas.
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PROSTIE: PSOGOGO, B RETOACYL SYNTHASE; 2.
PROSTIE: PSOGOGO, B RETOACYL SYNTHASE; 2.
PROSTIE; PSOIO12; PHOSPHOPANTETHEINE; 1.
COMPLETE PROSTIES: PSOILE2; QOR ZETA CRYSTAL; 1.
COMPLETE PSOILES; PSOSPHORANTETHEINE; Transferase.
SEQUENCE 3970 AA; 412662 MW; A93E583FAFA68C47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   on a Pseudomonas aeruginosa clone.";
J. Bacteriol. 184:6665-6680(2002).
EMBL. AF4405213. AAN62162.1;
-...
SEQUENCE 245 AA, 27314 MW, 86DA12B9069ACA7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NAR-2003 (TrEWBLrel. 23, Created)
01-NAR-2003 (TrEWBLrel. 23, Last sequence update)
Hypothetical protein ORF C68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245 AA
    21:526-531(2003).
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MEDLINE=22313472; PubMed=12426355;
Nat. Biotechnol. 21:526-531(200
EMBL; AB070340; BAB69199.1; -.
EMBL; AP005032; BAC70603.1; -.
HSSP; P25715; 1MLA
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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Q8GQ42;
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02-MAR-2004 (TEMBLrel. 27, Created)
02-MAR-2004 (TEMBLrel. 27, Last sequence update)
05-MAR-2004 (TEMBLrel. 27, Last sequence update)
05-MAR-2012 (TEMBLrel. 27, Last sequence update)
05-MAR-2012 (TEMBLrel. 27, Last sequence update)
05-MAR-2012 (TEMBLRel. 27, Last sequence update)
07-MAR-2012 (TEMBLRel. 27, Last sequence update)
07-MAR-2012 (TEMBLRel. 27, Last sequence update)
07-MAR-2012 (TEMBLRel. 27, Last sequence update)
07-MAR-2014 (TEMBLRel. 27, Last sequence
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Query Match 50.0%; Score 51; DB 2; Length 512; Best Local Similarity 53.3%; Pred. No. 39; Matches 8; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.0%; Score 51; DB 2; Length 512; 53.3%; Pred. No. 39; 6; Indels ive 1; Mismatches 6; Indels
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Sasaki T., Matsunco T., Katayose Y.;
Sasaki T., Matsunco T., Katayose Y.;
Curyza sativa nipponbare(GA3) genomic DNA, chromosome 8, 10ne:OSJNBa0016N23:";
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AP006049; BAD10739:1; -7813DC1C3B5FB4D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      512 AA
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Q25425
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6 DRVLEEWGLEPRQ 18

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Gaps

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49.0%; Score 50; DB 2; Length 288; 58.8%; Pred. No. 31; tive 2; Mismatches 5; Indels

Query Match
Best Local Similarity 58.88
Matches 10; Conservative

1 RGLWVDRVLEEWGLEPR 17

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EMBL; AP000061; BAA80533.1; -.
PIR; G72634; G72634.
Complete proteome; Hypothetical protein.
SEQUENCE 288 Aa; 32176 MW; 40235FA12BDD6APB CRC64;

8 % % S

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GO; 00:0016021; C:integral to membrane; IEA.
GO; 00:0016021; C:integral to membrane; IEA.
GO; GO:0004009; P:ATP binding: IEA.
GO; GO:0004009; P:ATP-binding cassette (ABC) transporter acti. . .; IEA.
GO; GO:000166; F:Nucleotide binding; IEA.
InterPro; IPR011527; ABC membrane 1.
InterPro; IPR011527; ABC membrane 1.
InterPro; IPR001140; ABC membrane 1.
InterPro; IPR00139; ABC membrane 1.
Pfam; PF00664; ABC membrane; 2.
Pfam; PF00665; ABC membrane; 2.
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                                                                                                                                      P-glycoprotein.
Leishmania tarentolae (Sauroleishmania tarentolae).
Eukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania;
NCBI_TaxID=5689;
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Pred. No. 1.38+02;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  Legare D., Hettema B., Ouellette M.;
"The P-glycoprotein-related gene family in Leishmania.";
Mol. Biochem. Parasitol. 68:81-91(1994).
-!- SIMILARITY: Belongs to the ABC transporter family.
EMBL; L29488; AAA65541.1; -.
PIR; T18343; T18343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1724 AA; 188967 MW; A8FE6CD4A65FA195 CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein APB1534.
OrderedLocusNames=APB1534;
                                                                                          (TrEMBLrel. 01, Last sequence update) (TrEMBLrel. 25, Last annotation update)
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PRT; 1724 AA.
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PROSITE; PSO0211; ABC_TRANSPORTER_1; 2.
PROSITE; PSS0893; ABC_TRANSPORTER_2; 2.
                                                                 Created)
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MEDLINE=95198776; PubMed=7891750;
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NCBI TaxID=56636;
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                                                              (TrEMBLrel. 01,
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Best Local Similarity 57.17
Best Local 8; Conservative
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      PRELIMINARY;
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                                                              01-NOV-1996
01-NOV-1996
                                                                                                                      01-OCT-2003
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                                  025425;
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         025425
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Chen C.-Y., Wu K.-H., Chang Y.-C., Chang C.-H., Tsai H.-C.,
Chen C.-Y., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
"Comparative genome analysis of Vibrio vulnificus, a marine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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STRAIN=CMCP6;
Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
Choy H.E.;
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EMBL, APRO5334; BAC93987.1; -.

GO, GO:000367; F:DNA binding! IEA.

GO, GO:0003887; F:DNA directed DNA polymerase activity; IEA.

GO, GO:0006260; P:DNA replication; IEA.

InterPro; IPRO04013; PHP_C.

InterPro; IPRO04013; PHP_C.

Pfam; PPC0231; PHP_C.

Pfam; PPC0231; PHP_C.

SEQUENCE 293 AA; 33152 MW; 62C1C56AF17720BC CRC64;
                                                                                                                                                                           Name=VV1223;
Vibrio vulnificus (strain YJ016).
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49.0%; Score 50; DB 2; Length 293; 50.0%; Pred. No. 31; ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last amnotation update)
predicted metal-dependent phosphoesterases.
                                                                                                              01-WAR-2004 (TrEMBLrel. 26, Created)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                   293 AA.
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                                                                                                                                                           Predicted metal-dependent phosphoesterase
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151 RGLGSDRVVAEWWLDSR 167
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les 10; Conservative
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                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                         pathogen.";
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                                                                                   Q7MM50
Q7MM50;
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Matches
                                                       RESULT 11
Q7MM50
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49.0%;
83.3%;
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Best Local Similarity 83.3%;
Matches 10; Conservative
              PROSITE, PS50885; HAMP; 1.
PROSITE, PS50113; PAC; 1.
PROSITE; PS50112; PAS; 1.
SEQUENCE 842 AA; 92860
                                                                                                          Query Match
Best Local Similarity 83.3
                                                                                                                                                                                                                                                          680 VDRVLEETGLDP 691
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STRAIN=PCA / ATCC 51573;
PubMed=14671304;
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NCBI_TaxID=171101;
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STRAIN-PCA / ATCC 51573;

STRAIN-PCA / ATCC 51573;

STRAIN-PCA / ATCC 51573;

STRAIN-PCA / ATCC 51573;

STRAIN-PCA / ATCC 51676;

Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,

Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,

Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,

Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,

Davidsen T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,

Weidman J.F., Khouri H.M., Feldblyum T.V., Utterback T.R.,

Van Aken S.E., Lovley D.R., Braser C.M.,

"Genome of Geobacter sulfurreducens: metal reduction in subsurface
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Geobacter sulfurreducens.
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
Geobacteraceae; Geobacter.
"Complete genome sequence of Vibrio vulnificus CMCP6.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.

R GO; GO:0003677; AAO11387.1;
R GO; GO:0003677; F:DNA binding; IEA.

R GO; GO:0005267; F:DNA-directed DNA polymerase activity; IEA.

R GO; GO:0005267; F:DNA-directed DNA polymerase activity; IEA.

R InterPro; IPR003141; Pesterase_FHP_N.

InterPro; IPR003141; Pesterase_FHP_N.

R Pfam; PF0231; PHP_C;

R Pfam; PF0231; PHP_N; 1.

R SMART; SMO4481; POLITIAC; 1.

R GMART; SMO4481; POLITIAC; 1.

R COMplete protecome.

O SEQUENCE 293 AA; 33178 MW; 5839B6813C495140 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                4,
                                                                                                                                                                                                                                                                                                                                             / Match 49.0%; Score 50; DB 2; Length 293; Local Similarity 50.0%; Pred. No. 31; les 10; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            074EL6,
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Sensory box/GGDEF family protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                842 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWART; SMO0304; HAMP; 1.
SWART; SMO0006; PAC; 1.
SWART; SMO0091; PAS; 1
TIGREAMS; TIGR00254; GGDEF; 1.
TIGREAMS; TIGR00254; Sensory_box; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              260 RNLWLPAGVEPVWKDWGLEP 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001610; PAC.
InterPro; IPR000014; PAS.
InterPro; IPR000700; PAS-assoc_C.
PEam; PF00563; BAL; 1.
PEam; PF00690; GGDEF; 1.
PEam; PF00672; HAMP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RGLW----VDRVLEEWGLEP 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                environments.";
Science 302:1967-1969(2003).
EMBL, AE017180; AAR34273.1; -
TIGR; GSU0946; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001633; EAL.
InterPro; IPR00160; GGDEF.
InterPro; IPR003660; HAMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50883; EAL; 1.
PROSITE; PS50887; GGDEF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00785; PAC; 1.
Pfam; PF00989; PAS; 1.
SWART; SW00267; DUF1; 1.
SWART; SW00052; DUF2; 1.
SWART; SW00304; HAMP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORFNames=GSU0946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=35554;
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                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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MEDLINE=21429245; PubMed=11544234;
Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S.,
DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,
Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Geobacter sulfurreducens.
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
Geobacteraceae; Geobacter.
Not I_TaxID=35554;
                                                                                                                        .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .,
                                                            2; Length 842;
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Pred. No. 91;
                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
842 AA; 92860 MW; 989697FE4637E9AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            842 AA; 92860 MW; 989697FE4637E9AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         02-WAR-2004 (TrEMBLrel. 27, Created)
02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
Sensory box/GGDEF family protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QBDQQ8;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein spr0544.
                                                         Score 50; DB 2; Pred. No. 91; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
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RA LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,
RA McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I.,
RA Sun P., O'Gara M., Peery R.B., Robertson G.T., Rockey P.,
RA Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud D.L.,
RA Glass J.I.;
RA Glass J.I.;
RA Glass J.I.;
RA Glass J.I.;
REL, AEOGRA31, ARX9348.1;
J. Bacteriol. 183:5709-5717(2001).
REL, AEOGRA31, ARX9348.1;
DR PIR, H97939; H9739.
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR InterPro: IPRO04843, Mypsterase activity; IEA.
DR InterPro: IPRO04843, Mypsterase activity.
DR PIRSP: PIRSPONDED: Thtase apaH.
DR PIRSP: PIRSPONDED: Thtase apaH.
DR PRER; PIRSPOND83; Peeterase apaH.
DR PRER; PIRSPOND83; Peeterase apaH.
DR PRODOM; PD000252; Thtase apaH.
SQ SEQUENCE 277 AA; Pred. No. 42;
Matches 12; Conservative 2; Mismatches 4; Indels 4; Gaps 1;

QV 1 RGLWVDRVLE---EWGLERPRQ 18
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Search completed: November 10, 2004, 14:50:36 Job time: 25.9774 secs

63 RGNWDDRVLEALDGQYGLEDPQ 84

8 8 us-10-092-750-64.rai

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Sequence 5476, Ap Sequence 5323, Ap Sequence 313, App Sequence 11, Appl Sequence 51, Appl Sequence 52, Appl Sequence 676, Appl Sequence 1662, A Sequence 15, Appl Sequence 55, Appl Sequence 55, Appl Sequence 55, Appl Sequence 56, Appl Sequence 51, Appli Sequence 61, Appli 61, App
                                                                                                                                                                        November 10, 2004, 14:55:47; Search time 12.9537 Seconds (without alignments) 143.349 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Issued Patents AA:*

(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-328-352-5476
US-09-543-681A-5323
US-09-1328-681A-5323
US-09-1328-672A-918
US-09-072-274-18
US-08-469-486-52
US-08-469-685-52
US-09-252-991A-16662
US-09-252-991A-16662
US-09-252-991A-25635
US-09-252-991A-25635
US-09-252-991A-25635
US-08-924-695A-55
US-08-924-695A-55
US-08-924-695A-55
US-08-924-695A-55
US-08-924-695A-52
US-08-924-695A-52
US-08-924-695A-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                      US-10-092-750-64
157
1 FVRSVGWRLQNIGDDMDHAICGHDVRLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                478139 seqs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47.5
47.5
47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
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                                                                                                                                                                                  Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Result
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Sequence 132, App Sequence 132, App Sequence 22906, A Sequence 2, Appli Sequence 2, Appli Sequence 24228, A Sequence 24228, A Sequence 23079, A Sequence 2311, Ap Patent No. 5183745 Sequence 2, Appli Patent No. 5183745 Sequence 2, Appli Sequence 8, Appl US-09-270-767-43062 US-08-961-083-132 US-09-58-084-132 US-09-582-991A-22906 US-09-922-937-2 US-09-922-917-2 US-09-252-991A-30608 US-09-252-991A-26428 US-09-252-991A-26418 US-09-252-991A-26419 US-09-252-991A-26419 US-09-252-991A-26419 US-09-252-991A-26419 US-08-669-785-2 US-08-669-785-2 US-08-669-785-2 US-08-669-785-2 US-08-669-785-2 US-08-03-741B-85 US-08-03-741B-85 US-08-03-741B-85 22666666666666444444 2001264666666444444

## ALIGNMENTS

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RESULT 2
US-09-543-681A-5323
US-09-543-681A-5323
US-09-543-681A-5323
Sequence 5323, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE REPERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
FILE REPERENCE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR PRIOR APPLICATION NUMBER: US 60/128,706
                                                                                                         APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NOS: 8252
BENTH: 614
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0
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Pred. No. 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 50; DB 4
Pred. No. 2;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Mismatches
US-09-328-352-5476

Sequence 5476, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           289 GWKIETVGDDIAWIKPGEDGRL 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27
                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 GWRLQNIGDDMDHAICGHDVRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 33.1%;
Best Local Similarity 40.9%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 55.6%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT; ORGANISM: Proteus mirabilis
US-09-543-681A-5323
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Gaps

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Query Match
30.6%; Score 48; DB 4; Length 375;
Best Local Similarity 52.9%; Pred. No. 22;
Matches 9; Conservative 4; Mismatches 4; Indels
                                                                                                           CUMPAIR.

ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTARRE: BAREAIT Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,433
FILING DATE: 04-MAY-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: CAITOIL, PECE G.
REGISTATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 37,834
TELEPHOMIN: (415) 705-8410
TELEPHOMIN: (415) 705-8410
TELEPHOMIN: (415) 397-8338
INFORMATION EN SEQ ID NO: 18:
SEQUENCE CHRACTERISTICS:
LENGTH: 375 amino acids

WINTER AND AND ACIDS AND ACIDS

LENGTH: 375 amino acids
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APPLICANT: Summers, R.G.
APPLICANT: Summers, R.G.
APPLICANT: Staver, L.
APPLICANT: Staver, M.J.
TITLE OF INVENTION: POLYKETIDE-ASSOCIATED SUGAR ITTLE OF INVENTION: BIOSYNTHESIS GENES ORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: 111inois
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRESEMO VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/576,626A
FILING DATE: 21-DEC-1995
CLASSIPICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dianne Casuto
                  FIRET: 220 mo.c.,
CITY: San Francisco
CITY: California
CINTE: California
CINTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 31, Application US/08576626A
, Patent No. 5998194
, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :||| || || |:::| |
244 TVGWPLQPILDNIEHLI 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 SVGWRLQNIGDDMDHAI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 375 amino acids
TYPE: amino acid
STRANDEDNESS: not releve
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: protein US-09-072-433-18
                                    STATE: Califo
STATE: Califo
COUNTRY: Uni
TE: 94104
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                                                                                                                                                                             18-05-198-452A-918
Sequence 918, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
TITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: 6849
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT PILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
LENGTH: 579
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US-09-323-872A-33

Sequence 33, Application US/09323872A

Parent No. 6395539

GREERAL INFORMATION:
PRICE OF INTERIOR INTERIOR: Compositions and Methods for Bioremediation
PILE REFERENCE: OHU-0364

CURRENT APPLICATION NUMBER: US/09/323,872A

CURRENT APPLICATION NUMBER: 09/072,433

PRIOR APLICATION NUMBER: 09/072,433

PRIOR PILING DATE: 1998-05-04

NUMBER OF SEQ ID NOS: 58

SOFTWARE: PatentIn version 3.0

LENGTH: 375

TYPE: PRI

CRADIENT 375

TYPE: PRI

CRADIENT 375

CORGANISM: Thauera aromatica
US-09-323-872A-33
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31.8%; Score 50; DB 4; Length 579;
Best Local Similarity 45.5%; Pred. No. 17;
Matches 10; Conservative 4; Mismatches 8; Indels
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Pred. No. 22;
4; Mismatches 4; Indels
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Patent No. 6551814
GENERAL INFORMATION:
APPLICANT: Coschigano, Peter W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ITLE OF INVENTION: BIRREMEDIATION
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 GWKIECIGDDIAWIRPGRDGRL 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 GWRLONIGDDMDHAICGHDVRL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 TVGWPLQPILDNIEHLI 260
                                    1 FVRSVGWRLQNIGDDMDH 18
                                                            71 FTRTVGCPCANIGDHADH 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 30.6%;
Best Local Similarity 52.9%;
Matches 9; Conservative
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US-09-072-433-18
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Gaps

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Best Local Similarity 39.19
Matches 9; Conservative
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US-09-679-279-16
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APPLICANT: Thosersen, Hans Christian
APPLICANT: Holtet, Thor Las
APPLICANT: Exzerodt, Michael
TITLE OF INVENTION: Improved method for the refolding of
TITLE OF INVENTION: proteins
NUMBER OP SEQUENCES: 58
CORRESPONDENCES: 58
CORRESPONDENCES: 58
CORRESPONDENCES: 58
CORRESPONDENCES: 61
CITY: Boston
STATE: 225 Franklin Street
CITY: Boston
STATE: USA
                                                                                                                                                                                                                                                                                                              Query Match 30.6%; Score 40; DB 2; Length 1114; Best Local Similarity 34.8%; Pred. No. 75; Matches 8; Conservative 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version
SOFTWARE: #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE TON NOTIONS:

REFERENCE TON NOTION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617 542 8906

TELER: 200154

INFORMATION FOR SEQ ID NO: 52:

LENGTH: 4544 amino acids
               REFERENCE/DOCKET NUMBER: 5857.US.O1
TELECOMUNICATION INFORMATION:
TELEPHONE: (847) 938-2623
TELEFAX: (847) 938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
                                                                                                                                                                                                                                                                                                                                                                                              2 VRSVGWRLQNIGDDMDHAICGHD 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 52, Application US/08469486
Patent No. 5739281
GENERAL INFORMATION:
P-40,943
                                                                                                                     INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 1114 amino acids
TYPE: amino acid
                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: No. 5998194e
                                                                                                                                                                                                        STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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                                                                                                                                                                                                                                                                    US-08-576-626A-31
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DB 1; Length 4544;

30.3%; Score 47.5;

Query Match

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                                                                                                                                                                                                                    Sequence 52, Application US/08469658
Patent No. 5917018
Patent No. 5917018
Patent INFORMATION:
PAPLICANT: The gersen, Hans Christian
APPLICANT: Excarodt, Michael
PITLE OF INVENTION: IMPROVED METHOD FOR THE REFOLDING OF
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

30.3%; Score 47.5; DB 2; Length 4544;
Best Local Similarity 39.1%; Pred. No. 4.5e+02;
Matches 9; Conservative 3; Mismatches 8; Indels 3.
                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: MASAGINABELES
CONTRY: USA
ZIP: 02110-2804
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,658
FILING DATE: Unme 5, 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/192.060
FILING DATE: February 4, 1994
CLASSIFICATION: 530
ATTORNEY/AGENT INCORMATION:
NAWE: Paul T. Clark
REGISTRATION: WUMBER: 30,162
REGISTRATION: WIMBER: 30,162
REGISTRATION NUMBER: 30,162
Pred. No. 4.56
3; Mismatches
                                                                                                991 NINWRCDNDDCGDNSDEAGCSH 1013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELERX: 617 542 8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 4544 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070
TELEFAX: 617 542 8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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## Sequence 25635, Application US/09252991A
## Sequence 25635, Application US/09252991A
## Sequence 25635, Application US/09252991A
## Patent No. 6551795
## Sequence 25635, Application
## PATENT NO. 6551795
## SPELICATION
## SET OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
## TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
## TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
## FILE REFERENCE: 10799-02-18
## CURRENT FILING DATE: 10799-02-18
## PRIOR FILING DATE: 10798-02-18
## PRIOR FILING DATE: 1078-02-18
## PRIOR FILING DATE: 1078-07-27
## NUMBER OF SEQ ID NOS: 33142
## PRIOR FILING DATE: 1078-07-27
## PR
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| FALENT NO. 0. 1.2260
| APPLICANT: Huang, Ziwei
| APPLICANT: Wang, Jialun
| APPLICANT: Zhang, Zhijia
| APPLICANT: Zhang, Zhijia
| APPLICANT: Shan, Simei
| APPLICANT: Shan, Simei
| APPLICANT: Shan, Simei
| TILE REFERENCE: 8321-6
| CURRENT APPLICATION NUMBER: US/09/544,664B
| CURRENT FILING DATE: 2000-04-06
| PRIOR APPLICATION NUMBER: PCT/US00/09352
| PRIOR PILING DATE: 2000-04-06
| PRIOR FILING DATE: 1999-04-07
| NUMBER OF SEQ ID NOS: 58
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
29.9%; Score 47; DB 4; Length 934;
Best Local Similarity 40.0%; Pred. No. 88;
Matches 10; Conservative 5; Mismatches 10; Indels
                                                            DB 4; Length 465; 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.3%; Score 46; DB 4; Length 27
                                                                                                                                   3; Indels
                                                                                                                                   4; Mismatches
                                                                      Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            800 QSVEWRLRQVGHDLLELLEHQDVPL 824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                      29.9%;
53.3%;
                                                                                                                                                                                                                                      276 RSEGWNLESLGLDMN 290
                                                                                                                                                                                                      3 RSVGWRLQNIGDDMD 17
                                                                   Query Match 29.9
Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         US-09-252-991A-25635
   US-09-252-991A-16662
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Sequence 16662, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOWONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERRNCE: 107196.136

CURRENT FILING DATE: 1999-02-18

PRIOR PILING DATE: 1999-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

SEQ ID NOS: 33142

LENGTH: 465
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Retent No. 6562958
GENERAL INFORMATION:
APPLICANT GARY L. Breton et al.
APPLICANT GARY L. Breton et al.
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRESENTE: G729-0378
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT PILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
LENGTH: 366
LENGTH: 366
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TITLE OF INVENTION: Recombinant Megalomicin Biosynthetic;
TITLE OF INVENTION: Genes and Uses Thereof
FILE REPERBENCE: 300622004700
CURRENT APPLICATION NUMBER: US 09/679,279
CURRENT FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/158,305
PRIOR PILING DATE: 1999-10-08
PRIOR PILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.9%; Score 47; DB 4; Length 366; 34.6%; Pred. No. 30; ive 7; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
29.9%; Score 47; DB 4; Length 358;
Best Local Similarity 34.8%; Pred. No. 29;
Matches 8; Conservative 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 RSVGWRLQNIGDDMDHAICGHDVRLG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT , ORGANISM: Micromonospora megalomicea US-09-679-279-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VRSVGWRLQNIGDDMDHAICGHD 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 34.6
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-09-252-991A-16662
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/924,695A
FILING DATE: 09-58P-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R:
REGISTRACE/DOCKET NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 35,197
REGISTRACE (314) 727-5188
TELEPRAK: (314) 727-5188
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 55:
INFORMATION FOR 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: November 10, 2004, 15:57:18 Job time : 12.9537 secs
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Best Local Similarity 42.1%;
Matches 8; Conservative
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TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-924-695A-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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1 Sequence 55, Application US/08706741B

1 Patent No. 595593

2 GENERAL INPORMATION:

1 TILLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST

NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDERSS:

ADDRESSEE: HOWELL & HAPERKAMP, L.C.

STREET: 7733 FORSYTH BLVD., SUITE 1400

CITY: ST. LOUIS

STATE: MISSOUR

COUNTRY: USA

ZIP: 63146

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/706,741B

FILING DATE: 09-SEP-1996

CLASSIFICATION INDERRI SECON

MAME: HOLLAND, DONALD R.

REFERENCE/DOCKET NUMBER: 965017

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFRANE: (314) 727-6188

TELEFRANE: MAMBER: US/08/51
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US-08-924-695A-55
US-08-924-695A-55
; Sequence 55, Application US/08924695A
; Patent No. 5998583
; GENERAL INCOPMATION:
; TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
; STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 46; DB 2; Length 32;
Pred. No. 2.6:
                                     7; Indels
Best Local Similarity 42.1%; Pred. No. 2.1;
Matches 8; Conservative 4; Mismatches
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                                                                                                     2 VRSVGWRLQNIGDDMDHAI 20
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IHNIARHLAQIGDEMDHNI 23
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Best Local Similarity 42.1%;
Matches 8; Conservative
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TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: peptide US-08-706-7418-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 63105
COMPUTER READABLE FORM:
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US-08-706-741B-55
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Gaps

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7; Indels

4; Mismatches

Score 46; DB 2; Length 32; Pred. No. 2.6;

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Sequence 5, Appli

US-09-272-975-5

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                                                                                                                                                                                   November 11, 2004, 02:43:24 ; Search time 67.6584 Seconds (without alignments) 146.426 Million cell updates/sec
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2: /cgn2_6/ptodata/2/pubpaa/PCT_REAP_UBL.pep:*

3: /cgn2_6/ptodata/2/pubpaa/PCT_REAP_UBL.pep:*

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6: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUBL.pep:*

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10: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*

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19: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
                          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                              US-10-092-750-64
157
1 FVRSVGWRLQNIGDDMDHAICGHDVRLG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1568699 seqs, 353819137 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

 Result
 Query

 No.
 Score
 Match Length DB
 ID

 1
 157
 100.0
 28
 14
 US-10-039-750-64
 Sequence 64, Appl 2

 2
 1
 38.2
 526
 15
 US-10-739-237510
 Sequence 7444, Appl 38.2

 4
 60
 38.2
 526
 15
 US-10-424-599-247510
 Sequence 247510, Appl 37.6

 5
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 148
 15
 US-10-424-599-22598
 Sequence 245598, Appl 455, Appl 457, Appl 47.6

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 Sequence 216598, Appl 47.6

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 US-10-424-599-246092
 Sequence 216598, Appl 47.6

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 US-10-424-599-246092
 Sequence 216692, Appl 47.6

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 34.4
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 US-10-424-599-218856
 Sequence 216692, Appl 47.6

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 54
 34.4
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 17
 US-10-424-599-218856
 Sequence 216692, Appl 47.6

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APPLICANT: Lessa Thomas J
APPLICANT: Availa David K
APPLICANT: Availa David K
APPLICANT: Show Yinua
APPLICANT: Show Yinua
APPLICANT: Cao Yongwa Vinua
APPLICANT: Cao Yongwa Vinua
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICANION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
ENG ID NO 235298
LENGTH: 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: KOVALIC, DAVIG K.

TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53377) B
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
SEQ ID NO 9193
LENGTH: 332
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Pred. No. 2.8;
4; Mismatches 8; Indels
                                                                                                                                                                                                  Length 532;
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US-10-424-599-235298
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US-10-739-930-9193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 37.6%; Score 59; DB 15; Best Local Similarity 42.9%; Pred. No. 1.2; Matches 9; Conservative 4; Mismatches 8
                                                                                                                                                                                                  Query Match 38.2%; Score 60; DB 15; Best Local Similarity 54.5%; Pred. No. 3.2; Matches 12; Conservative 1; Mismatches 9
                                                                                                                           ; OTHER INFORMATION: Clone ID: 700953440_FLI.pep
US-10-425-114-49445
                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-10-444-599-235298
Sequence 235298, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9193, Application US/10739930 Publication No. US20040216190A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   316 GWRTNRİGDDGLHAİAKHCLNL 337
                                                                                                                                                                                                                                                                                                 6 GWRLQNIGDDMDHAICGHDVRL 27
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Best Local Similarity 42.9%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Glycine max
                            LENGTH: 532
TYPE: PRT
ORGANISM: Glycine max
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US-10-739-930-9193
  SEQ ID NO 49445
LENGTH: 532
                                                                                                      FEATURE:
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| Sequence 247510, Application US/10424599
| Sequence 247510, Application US/2A1
| GENERAL INFORMATION:
| APPLICANT: La Rosa Thomas J
| APPLICANT: Cao Yongwei I
| TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement |
| TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement |
| FILE REPRENCE: 38-21(5223)8 |
| CURRENT PLING DATE: 2003-04-28 |
| NUMBER OF SEQ ID NOS: 285684 |
| SEQ ID NO 247510 |
| LENGTH: 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: UNDBER: US/10/425,114
CURRENT FILLING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
APPLICANT: Kovalic, David K.

TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21 (5.3377) B
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
SEQ ID NOS: 11088
LENGTH: 381
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Pred. No. 1.6;
1; Mismatches 9; Indels
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                                                                                                                                                                                                                                                                            FEATURE:
; OTHER INFORMATION: Clone ID: ZEAMA-23APR03-C152384_1.p
US-10-739-930-7444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , OTHER INFORMATION: Clone ID: PAT_MRT3847_65530C.1.pep
US-10-424-599-247510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38.2%; Score 60; DB 15;
Best Local Similarity 54.5%; Pred. No. 3.2;
Matches 12; Conservative 1; Mismatchen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               310 GWRTNRIGDDGLHAIAKHCLNL 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FVRSVGWRLQNIGDDMDHAIC 21
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 52.4%;
Matches 11; Conservative
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1 FVRSVGWRLQNIGDDMDHAIC 21

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US=0.425-115-286505

i Sequence 286505, Application US/10425115

i Sequence 286505, Application US/10425115

i Publication No. US20040214272A1

i GENERAL INFORMATION:

i APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

i APPLICANT: Zhou, Yihua

i APPLICANT: Cao, Yongwei

i TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

ITILE OF INVENTION: Plants

ITILE OF INVENTION: Plants

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

i ENGTH: 1551
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Publication No. US20040031072A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILLE REFRENCE: 38-21(5123)B
CURRENT APPLICANT: APPLICANT: 2003-04-28

FILLE REFRENCE: 38-21(5123)B
CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT PILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

LENGTH: 124
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Best Local Similarity 42.1%; Pred. No. 73;
Matches 8; Conservative 7; Mismatches 4; Indels (
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_109464C.1.pep
US-10-424-599-153311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Zea mays PEATURE: ORGANISM: OPEATURE: OTHER INFORMATION: Clone ID: MRT4577_24390C.1.pep US-10-425-115-28650S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 50976, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 IRITSWRLSVLGPGSTHSQCGDD 53
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|1104 VRAVRWRLKDLGTEVPHCV 1122
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APPLICANT: Zamidio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
US-10-282-122A-50976
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US-10-424-599-153311
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                                                                                                                                                                                                                  Sequence 246092, Application US/10424599
Sequence 246092, Application US/2040031072A1
Sequence 246092, Application NS/2040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
Thou Yihua
APPLICANT:
Cao Yongwei
TITLE OF INVENTION:
Plants and Uses Thereof for Plant Improvement
FILE SEPREMENCE: 38-21(5323)3
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 246092
LIBNGTH: 341
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US-10-424-599-218856
US-10-424-599-218856
Sequence 218856, Application US/10424599
Fublication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: VIOLATION OF SECTION                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 35.0%; Score 55; DB 15; Length 341; Best Local Similarity 38.1%; Pred. No. 11; Matches 8; Conservative 4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COTATION: (1)..(479)
COTHER INFORMATION: unsure at all Xaa locations
FEATURE:
FEATURE:
COTHER INFORMATION: Clone ID: FAT_MRT3847_39655C.1.pep
US-10-424-599-218856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: PAT_MRT3847_64251C.1.pep
US-10-424-599-246092
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                                       221 FAEKVGWKIQKRDEDLIHEIC 241
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ORGANISM: Glycine max
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ORGANISM: Glycine max
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Fri Nov 12 14:55:52 2004

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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Excellic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Bunkharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: No. Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 137212
Query Match 33.8%; Score 53; DB 14; Length 604; Best Local Similarity 45.5%; Pred. No. 39; Matches 10; Conservative 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) OTHER INFORMATION: Clone ID: PAT_MRT4530_38716C.1.pep
US-10-437-963-137212
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 137212, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
                                                                                                                                                                                                       6 GWRLQNIGDDMDHAICGHDVRL 27
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US-10-437-963-137212
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-03-20
PRIOR PLING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR PELICATION NUMBER: 60/207,727
PRIOR PLING DATE: 2000-05-26
PRIOR PELICATION NUMBER: 60/230,335
PRIOR PLING DATE: 2000-05-66
PRIOR PLING DATE: 2000-05-06
PRIOR PLING DATE: 2000-05-06
PRIOR PLING DATE: 2000-05-06
PRIOR PLING DATE: 2000-010-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-110-23
PRIOR PLING DATE: 2000-110-23
PRIOR PLING DATE: 2000-110-29
PRIOR PLING DATE: 2000-110-29
PRIOR PLING DATE: 2000-110-29
PRIOR PLING DATE: 2000-110-29
PRIOR PLING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PLING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PLING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PLING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin version 3.1
SEQ ID NO 50976
LENGTH: 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Bordet
US-10-282-122A-50976
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0
Query Match 32.8%; Score 51.5; DB 16; Length 374; Best Local Similarity 43.5%; Pred. No. 40; Matches 10; Conservative 4; Mismatches 8; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Hendrickson, Ronald C.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: Houghton, Raymond L.
ITILE OF INVENTION: TUBERCILOSTS ANTIGENS AND METHODS
ITILE OF INVENTION: TUBERCILOSTS ANTIGENS AND METHODS
ITILE OF INVENTION: TUBERCILOSTS ANTIGENS AND METHODS
ITILE OF INVENTION: 1999-03-18
CURRENT APPLICATION WUMBER: US/09/272,975
CURRENT FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 45.5%; Score 51; DB 10;
Best Local Similarity 45.5%; Pred. No. 78;
Matches 10; Conservative 3; Mismatches 9
                                                                                                                      S VGWRLQNIGDDMDHAICGHDVRL 27
                                                                                                                                                                         56 VEWEFKSLEDGKMHA-CGHDVHV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) ORGANISM: Mycobacterium tuberculosis
US-09-272-975-5
                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09272975 Publication No. US20030027774A1
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; TYPE: PRT ; ORGANISM: Thermobifida fusca US-10-369-493-8112

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PD 287 GWRAETLGDDIAMMRFGKDGRL 308

RESULT 15
US-10-367-094-9
; Sequence 9, Application US/10367094
; Publication No. US20040170982A1
; GENERAL INFORMATION:
APPLICANT: David W. Morris
; APPLICANT: March Malandro
; TITLE OF INVENTION: WOVEL Therapeutic Targets in Cancer
; TITLE OF INVENTION: 000-00-1500
; UNRENT PILING DATE: 2003-02-14
; UNMERR OF SEQ ID NOS: 203
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; CURRENT #1.605
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-367-094-9

Query Match Milarity 44.4*; Pred. No. 92; Mismatches 12; Conservative 5; Mismatches 12; Conservative 5; Mismatches 11; Gaps 11;
Db 23 FFRGWHELFNUGDDWDHAICGHDVRL 27
Db 23 FFRGWHELFNUGDDV-YALPGSDINL 48
Search completed: November 11, 2004, 07:41:44
Job time: 67.6584 secs
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- protein search, using sw model OM protein

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

November 10, 2004, 14:52:32 ; Search time 9.56584 Seconds (without alignments) 281.634 Million cell updates/sec Run on:

US-10-092-750-64 157 1 FVRSVGWRLQNIGDDMDHAICGHDVRLG 28 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	probable pckA prot	phosphoenolpyruvat	probable phosphoen	hypothetical prote	frcB protein (AF19	probable phosphoen	phosphoenolpyruvat	phosphoenolpyruvat	phosphoenolpyruvat	probable potassium	hypothetical prote		_		phosphoenolpyruvat	hypothetical prote	hydroxyacylglutath	ornithine carbamoy	transcription fact	alpha-2-macroglobu	alpha-2-macroglobu	alpha-2-macroglobu	probable acetyltra	2	deh	F	probable L-a-amino		
ID	A70960	723	10	AB2584	B97366	$\overline{}$	N	A86597	JQ1462	C72692	G96940	G83689			A45625	T24168	AB3314	F82737	T10695	A53102	802392	825111	C75096	AB1943	F83365	1.1	2	AB0106	G70817
DB	2	N	0	~	7	N	~	N	N	N	N	N	N	N	~	N	Ŋ	(1)	N	Н	н	H	N	7	~	7	7	0	-
Length	909	609	618	340	340	599	900	009	608	295	786	108	262	492	619	654	218	336	833	4543	4544	4545	205	374	464	1249	199	285	372
% Query Match	32.5	N	N	н	<b>₹</b> -1	-1	-1	-1	н	$\vdash$	$\leftarrow$	0	0	0	О	О	0	0	0	0	0	0	σ	σ	σ	σ	σ	σ	S)
Score	51	51	51	20	20	20	20	20	50	49	49	48	48	48	48	48	٠	۲.	٠	7.	٠	7.	47	47	47	47	46	46	46
Result No.	п.	7	m	4	Ŋ	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

_ C!	NADH oxidase SS019	heat shock protein	phosphoenolpyruvat	hypothetical prote	fibulin, splice fo	fibulin, splice fo	SpoE family protei	cell division prot	gene 44 protein -	amino acid amidohy	Ig lambda chain pr	bacterioferritin c	conserved hypothet	probable f0-f0 par	MRP protein homolo
S44367	D90354	C83168	830180	T32875	S78040	S34968	D95101	E97969	WZBE44	B86660	A30554	B82742	E81672	T38680	A90191
0	~	N	(7	7	~	~	7	~	~	~	~	N	~	N	N
389	555	619	646	651	685	705	767	167	363	384	129	159	178	286	296
29.3	29.3	29.3	29.3	29.3	29.3	29.3	29.3	29.3	29.0	29.0	28.7	28.7	28.7	28.7	28.7
46	46	46	46	46	46	46	46	46	45.5	45.5	45	45	45	45	45
30	31	32	33		35	36		38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1
nrobable pckA protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: A70960
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon,
, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A, Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A; Reference number: A70500; MUID: 98295987; PMID: 9634230
A;Accession: A70960
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-606 < COL>
A; Cross-references: UNIPROT: P96393; GB: Z92669; GB: AL123456; NID: 93242271; PIDN: CAB07006
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: pckA
C;Superfāmily: phosphoenolpyruvate carboxykinase (GTP)
Onerv Match 32.5%; Score 51; DB 2; Length 606;

·. Gaps ö Indels σı ... 32.5%; Score 51; DB 45.5%; Pred. No. 13; tive 3; Mismatches 10; Conservative Query Match Best Local Similarity Matches

287 GWRAETLGDDIAWMRFGKDGRL 308 6 GWRLQNIGDDMDHAICGHDVRL 27 셤 ઠ

phosphoenolpyruvate carboxykinase [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004
C;Accession: F97237
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hamin, N.; Halloyd
eam, N.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S.
A;Atterence number: A66909; MUID:21126732; PMID:11234002
A;Accession: F87337
A;Accession: F87337
A;Accession: F87337
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-609 <STO>
A;Cross-references: UNIPROT:006084; GB:AL450380; NID:913093848; PIDN:CAC32156.1; GSPDB
C;Genetics:
A;Gene: pckA

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CjAcession: B97366
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Iuu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tur A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: B97366
A;Status: preliminary
A;Molecule type: DNA
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A,Status: preliminary
A,Molecule type: DNA
A,Molecule type: DNA
A,Cresidues: 1-599 - ARNS
A,Cresidues: 1-599 - ARNS
A,Eross-references: UNIPROT:084716, GB:AE001341; GB:AE001273; NID:g3329156, PIDN:AAC683
A,Experimental source: serotype D, strain UW-3/Cx
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A;Cross_references: UNIPROT:Q8UJ75; GB;AE007869; PIDN:AAK85883.1; PID:g15154926; GSPDB:
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C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23.Apr-1999 #sequence_revision 23.Apr-1999 #text_change 09-Jul-2004
C;Accession: E72021,
R;Kalma1, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood,
Nature Genet. 21, 385-389, 1599
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MuID:99206606; PMID:10192388
                                                                                                                                                                   frcB protein (AF196574) [imported] - Agrobacterium tumefaciens (strain C58, Cereon) C;Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
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C,Superfamily: phosphoenolpyruvate carboxykinase (GTP)
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Pred. No. 9.9;
2; Mismatches 8
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31.8%; Score 50; DB
Best Local Similarity 45.5%; Pred. No. 18;
Matches 10; Conservative 5; Mismatches
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A,Map position: circular chromosome
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Best Local Similarity 50.0%;
Matches 10; Conservative
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A, Molecule type: DNA
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Aolecule type: DNA
A;Residues: 1-618 <COL>
A;Coss-references: UNIPROT: 083159; GB:AE001197; GB:AE000520; NID:G3322382; PIDN:AAC6511
A;Coss-references: train Nichols
C;Genetics:
A;Gene: TP0122
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A,Experimental source: strain C58 (Dupont)
C,Genetics:
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R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDethey, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998

A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.

A;Reference number: A71250; MUID:98332770; PMID:9665876
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A'Itle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A'Reference number: AB2577; MUID:21608550; PMID:11743193

A'Accession: AB2584

A'Status: preliminary

A'MOlecule type: DNA

A'Residues: 1-340 < KUR>
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C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
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                                                                                 Query Match 32.5%; Score 51; DB 2; Length 609; Best Local Similarity 45.5%; Pred. No. 13; Matches 10; Conservative 3; Mismatches 9; Indels
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C; Superfamily: phosphoenolpyruvate carboxykinase (GTP)
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31.8%; Score 50; DB 2
Best Local Similarity 50.0%; Pred. No. 9.9;
Matches 10; Conservative 2; Mismatches
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287 GWRAETLGDDIAWMRFGKDGRL 308
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probable potassium channel APE0955 - Aeropyrum pernix (strain K1)
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C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Date: 0.1-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: G83689
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir Nucleic Acids Res. 28, 4317-431, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83689
A;Accession: G83689
A;Accessio
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A;Experimental source: strain C-125
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A,Experimental source: Clostridium acetobutylicum ATCC824
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Pred. No. 12;
5; Mismatches
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Best Local Similarity 55.6%;
Matches 10; Conservative
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A,Molecule type: DNA
A,Residues: 1-786 <KUR>
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A;Accessivant. A86597
A;Accessivant and A;Status: preliminary
A;Molecule type: DNA
A;Residuse: 1-60 o KSTO-
A;Acsiduse: 1-60 o KSTO-
A;Acsiduse: 1-60 o KSTO-
A;Across-references: UNIPROT:092755; GB:BA000008; NID:g8979225; PIDN:BAA99059.1; GSPDB:GN
A;Cross-references: UNIPROT:092755; GB:BA000008; NID:g8979225; PIDN:BAA99059.1; GSPDB:GN
A;Experimental source: strain J138
A;Experimental source: strain J138
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A,Residues: 1-600 <ARN>
A;Cross-references: UNIPROT:Q9Z755; GB:AE001666; GB:AE001363; NID:g4377164; PIDN:AAD1898
A;Experimental source: strain CWL029
C;Genetics:
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R.Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; E. Nucleic Acids Res. 28, 2311-2314, 2000
A.Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A.Reference number: A86491; MUID:20330349; PMID:10871362
A.Accession: A86597
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C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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Pred. No. 18;
4; Mismatches 8; Indels
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                                                                                A;Cross-references: UNIPROT:Q99755; GB:Abuulees; GB:Ab
A;Experimental source: strain CWL029
C;Genetics:
A;Gene: pckA
C;Superfamily: phosphoenolpyruvate carboxykinase (GTP)
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GWKIECIGDDIAWIRPGRDGRL 302
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A.Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A.Reference number: A84420; MUID:20083487; PMID:10617197
A.Accession: C84563
A.Status: preliminary
A.Reideule type: DNA
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C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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30.6%; Score 48; DB 2; Length 108;
Best Local Similarity 44.0%; Pred. No. 5.8;
Matches 11; Conservative 3; Mismatches 7; Indels
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33.3%; Pred. No. 15;
ive 4; Mismatches 10; Indels
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phosphoenolpyruvate carboxykinase (GTP) (EC 4.1.1.32) - nematode (Haemonchus contortus)
NyAlternate names: phosphoenolpyruvate carboxylase
C;Species: Haemonchus contoxtus
C;Species: Haemonchus contoxtus
C;Bpecies: Haemonchus contoxtus
C;Bte: 03-Fb-1994 #sequence_revision 03-Fb-1994 #text_change 09-Jul-2004
C;Accession: A45625
R;Ktein, R.D.; Winterrowd, C.A.; Hatzenbuhler, N.T.; Shea, M.H.; Favreau, M.A.; Nulf, S.
A;Title: Cloning of a cDNA encoding phosphoenolpyruvate carboxykinase from Haemonchus of A;Reference number: A45625, MulD: 92188009; PMID: 1741016
A;Accession: A45622
A;Actaus: preliminary
A;Resion: A45622
A;Actaus: preliminary
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A;Actaus: preliminary
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A;Accession: A45622
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A;Accession: A45622
A;Accession: A45622
A;Corsa-references: UNIPROT: P29190; GB:W76494; NID: GIS9182; PIDN: AAA29180.1; PID: GIS9182
A;Corsa-references: UNIPROT: P29190; GB:W76494; NID: GIS9182; PIDN: AAA29180.1; PID: GIS9182
A;Corsa-references: UNIPROT: P29190; GB:W76494; NID: GIS9182; PIDN: AAA29180.1; PID: GIS9182
A;Corsa-references: Carboxy-lyase; Garboxy-lyase; gluconeogenesis
C;Superfamily: phosphoenolpyruvate carboxy/kinase (GTP)
C;Superfamily: phosphoenolpyruvate carboxy/lyase; gluconeogenesis
C;Superfamily: phosphoenolpyruvate carboxy-lyase; gluconeogenesis
C;Superfam
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SEQUENCE FROM N.A.
STEATNE-type strain: DSM44215;
STRANNE-type strain: DSM44215;
Characterization of the 101.016 kbp megaplasmid pKB1 isolated from the rubber degrading bacterium Gordonia westfalica Kbl.";
Dacteriol. 186:212-225(2004).
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02-MAR-2004 (TrEMBLrel. 27, C)
02-MAR-2004 (TrEMBLrel. 27, Ls
02-MAR-2004 (TrEMBLrel. 27, Ls
Hypothetical protein.
Gordonia westfalica.
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05-JUL-2004
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Q7vs40 bordetella
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Q81hk8 dictyostelli
Q85j15 oryza sativ
Aar88567 oryza sativ
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QB81k0 pseudomonas
O84716 chlamydia t
Q92755 chlamydia p
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Cae09117 gordonia
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343.270 Million cell updates/sec
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                                                                                                           November 10, 2004, 14:50:40 ; Search time 46.9324 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1 FVRSVGWRLQNIGDDMDHAICGHDVRLG 28
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Maximum Match 100%
Listing first 45 summaries
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SYI THETH
Q72JR6
                                                                       using sw model
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Q874G3
Q7VS40
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1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                                                                                                                                                          seq length: 0
seq length: 200000000
                                                                                                                                                                                   US-10-092-750-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query
Match Length
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                                                                       - protein search,
                                                                                                                                                                                                                                                            BLOSUM62
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Perfect score:
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Maximum DB
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                                                                                                           Run on:
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Last sequence update) Last annotation update)

Created)

230 AA

PRT;

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ö
                   Q93jls streptomyce
Q7n6x2 photorhabdu
Q94fls aerobyum p
Q985p8 rhizobyum p
Q6mbf4 parachlamyd
Caf24095 parachlamyd
Q97m65 clostridium
Q6d580 erwinia car
Q8c9u6 mus musculu
Q8c9u6 mus musculu
Q8c9u6 mus musculu
Q8c9u6 yeadyrhizob
Q7xtv7 oryza sativ
Q3xtv7 oryza sativ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=type strain: DSM44215;
Brocker D., Arenskoetter M., Legatzki A., Nies D.H., Steinbuchel A.;
"Characterization of the 101.016 kbp megaplasmid pKB1 isolated from the rubber degrading bacterium Gordonia westfallca Kbl.";
J. Bacteriol. 186:212-225(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ·,
           P22130
Q93j15
                                                                                                                                                                                                                                                                                                  Bacteria; Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae; Gordoniaceae; Gordonia.
NCBL_TaxID=158898;
                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match
Local Similarity 45.8%; Pred. No. 0.96;
les 11; Conservative 3; Mismatches 10: Indels
                                                                                                                                                                                                                                                                                                                                                                                               J. Bacteriol. 186:212-225(2004).
EMBL. AJ576039, CAEOJ17.1, -
HYDOChetical protein; Plasmid.
SEQUENCE 230 AA; 25736 MW; 929260575B53D0F2 CRC64;
                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                    230 AA
                                                                                                                                                                  ALIGNMENTS
PPCK_STRAW
PPCK_NEOFR
PPCK_STRCO
Q7N6X2
                                       KVAP AERPE

Q985P8

Q6MBF4

CAF24095

Q6786

Q60580

Q8C9U6
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                                                                                                                                                                                                                                        Created)
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                                                                                                                         Q7XTV7
Q9KFZ7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FVRSVGWRLQNIGDDMDHAICGHD
                                                                                                                                                                                                                    PRELIMINARY;
 (TrEMBLrel.
                                                                                                                                                                                                                                                 (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                   Hypothetical protein.
Gordonia westfalica.
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662 RSLGIKITVTSDDSDESDEHDHAHGGHD 689
                                                                                                                                                                                                                               NCBI_TaxID=520;
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Q7W1Q3;
                                                                                      07VS40
                                                          RESULT 4
Q7VS40
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                 임
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:000367; F:DWA binding; IEA.
GO; GO:00046519; F:PMA binding; IEA.
GO; GO:00046933; F:hydrogen-transporting ATP synthase activity. .; IEA.
GO; GO:0016986; P:hydrogen-transporting ATP synthase activity. .; IEA.
GO; GO:0019986; P:hydrogen-transporting ATPase activity, rota. .; IEA.
GO; GO:0019986; P:protein splicing; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Okuda Y., Sasaki D., Nogami S., Kaneko Y., Ohya Y., Anraku Y.; "Occurrence, horizontal transfer and degeneration of VDE intein family in Saccharomycete yeasts."; Sasat 20:563-57312003.
-! SIMILARITY: Belongs to the ATPase alpha/beta chains family.
                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                   Brocker D.,
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ5/6039, CAE09117.1, -.
Helicase, Hypothetical protein, Lipoprotein, Methyltransferase;
                                                                                                                                                              .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34.4%; Score 54; DB 2; Length 1067; 42.9%; Pred. No. 52; tive 3; Mismatches 7; Indels
                                                                                                                             'Match 38.9%; Score 61; DB 2; Length 230; Local Similarity 45.8%; Pred. No. 0.96; les 11; Conservative 3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1067 AA; 116776 MW; 708BAE8DD5D9CDC1 CRC64;
                                                                                                     230 AA; 25736 MW; 929260575B53D0F2 CRC64;
                                                                                                                                                                                                                                                                                                                 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUNA-2004 (TrEMBLrel. 26, Last annocation update)
Vacuolar membrana ATPase subunit a 1 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000194; ATPase_a/bcentre.
InterPro; IPR000194; ATPase_a/b_C.
InterPro; IPR00190; ATPase_a/b_N.
InterPro; IPR001869; Hom_end.
InterPro; IPR007869; Hom_end.
InterPro; IPR007868; Hom_end. hint.
InterPro; IPR004042; Intein_endonuc.
Pfam; PP00306; ATP-synt_ab_1.
Pfam; PP00306; ATP-synt_ab_C; 1.
Pfam; PPC02106; ATP-synt_ab_C; 1.
Pfam; PPC02104; Hom_end, hint; 1.
Pfam; PPC02104; Hom_end, hint; 1.
PR09ITE; PS00152; ATPASE ALPHA BETA; UNKNOWN 1.
PR09ITE; PS00152; ATPASE ALPHA BETA; UNKNOWN 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22620229; PubMed=12734795;
                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces exiguus (Yeast)
       SEQUENCE FROM N.A.
STRAIN=type strain: DSM44215;
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Matches 12; Conservative
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SEQUENCE
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Q874G3;
                                                                                          Plasmid
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Matches
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SEQUENCE FROM N.A.

C STAIN=Tobnama I / ATCC BAA-589 / NCTC 13251;

MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

A Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,

A Harris D.E., Holden M.T.G., Churcher C.M., Beneley S.D., Mungall K.L.,

A Cachaon-Tarraga A. A., Temple L., James K.D., Harris B., Quail M.A.,

A Achtuan M., Akkin R., Baker S., Basham D., Bason N., Cherevach I.,

Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

A Fletwell T., Goble A., Handlin N., Hauser H., Holtoyd S., Jagels K.,

Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

A Rabbinowitsch B., Rutter S., Sanders M., Saunders D., Seeger K.,

Sharp S., Simmonds M., Skelton J., Squares S., Stevens K.,

A Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;

"Comparative analysis of the genome sequences of Bordetella pertussis,

"Comparative analysis of the genome sequences of Bordetella pertussis,

"Comparative analysis and Bordetella bronchiseptica.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=12822 / ATCC BAA-587;
MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,
Harris D.B., Holden M.I.G., Churcher C.M., Bentley S.D., Mungall K.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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NCBI_TaxID=519;
                                                                                                                                                                                                                          Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nat. Genet. 35:32-40(2003).
EMBL. BX640412; CAE44936.1; -.
GO; GO:0016779; F:nucleotidyltransferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome; Nucleotidyltransferase; Transferase.
SEQUENCE 264 AA; 28007 MW; CASBB10EFEC3D944 CRC64;
                                         01-007-2003 (TrEMBLrel. 25, Created)
01-007-2003 (TrEMBLrel. 25, Last sequence update)
01-07-2003 (TrEMBLrel. 26, Last annotation update)
Adenylyltransferase (EC 2.7.7.).
Name=thiF; OrderedLocusNames=BP0610;
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 26, Last annotation update)
Adenylyltransferase (EC 2.7.7.).
Name-thif; OrderedLocusNames=BPP0298;
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264 AA
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PRT;
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InterPro; IPR002205; MAD BS.
InterPro; IPR000594; ThiF domain.
Pfam; PP05237; MoeZ MoeB; 1.
Pfam; PP00899; ThiF; 1.
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Les 10, Conservative
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PRELIMINARY;
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3 RSVGWRLQNIGDDM-----DHAICGHD 24

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Indels

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47.68;

Conservative

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Best Local Similarity
Matches 10; Conserv
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SEQUENCE FROM N.A.

STAIN-RESO / ATCC BAA-588;

STRAIN-RESO / ATCC BAA-588;

STRAIN-RESO / ATCC BAA-588;

STRAIN-RESO / ATCC BAA-588;

Barkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,

Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall N.L.,

Cerdeno-Tarraga A.-M., Temple J., James K.D., Harris B., Quail M.A.,

Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

Achtman M., Atkin R., Cronin A., Davis P., Doggett J.,

Chillingworth T., Gollins M., Cronin A., Davis P., Doggett J.,

Reltherl T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

Annun L., Whitehead S., Barrell B.G., Maskell D.J.;

"Comparative analysis of the genome sequences of Bordetella pertussis,

"State Comparative analysis and Bordetella bronchiseptica.";
Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A., Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I., Chillingworth T., Collins M., Crointa A., Davis P., Dogett J., A. Chillingworth T., Collins M., Crointa A., Davis P., Dogett J., Callins M., Callins M., Davis P., Dogett J., Callins M., Callins M., Callins M., Davis P., Dogett J., Callins M., Callins M., Callins J., Davis R., Jagels K., Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C., Rabbinowitsch E., Rutter S., Sanders B., Seeger K., Dawin L., Whitehead S., Barrell B.G., Maskell D.J., Geger K., Unwin L., Whitehead S., Barrell B.G., Maskell D.J., Geger K., Comparative analysis of the genome sequences of Bordetella pertussis, Bordetella parapertussis and Bordetella bronchiseptica."; DAT GO; GO:0016779; Finalsefrase activity; IEA.

GO; GO:0016779; Finalsefrase activity; IEA.

InterPro; IPR007901; Noez MoeB.

InterPro; IPR000594; ThiF domain.

Pfam; PP005237; MoeZ MoeB.

Pfam; PP00899; ThiF Johnsin Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell D. Maskell 
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Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 264;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome, Nucleotidyltransferase, Transferase.
SEQUENCE 264 AA; 28094 MW; 1FC05B44B6A8BDC5 CRC64;
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EMBL, BX640437; CAE30799.1; CAE307999.1; CAE307999.1; CAE307999.1; CAE307999.1; CAE307999.1; CAE307999.1; CAE307999.1; CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MR-2004 (TrEMBLrel. 26, Last annotation update)
Adenylyltransferase (EC 2.7.7.).
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Pred. No. 17;
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NCBI TaxID=518;
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Best Local Similarity 47.67
Matches 10, Conservative
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Q7WQM9
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Length 264;

DB 2;

53;

33.8%; Score

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., CHARACTERIZATION, AND MASS SPECTROMETRY.
MEDLINE=121382897; PubMed=11278451; DOI: 10.74/jbc.M008960200;
MEDLINE=210382897; Concar E.M., Wolfe R.S.;
"A GTP-dependent vertebrate-type phosphoenolpyruvate carboxykinase from Mycobacterium mengmatis.",
J. Biol. Chem. 276:15137-16145(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Belongs to the phosphoenolpyruvate carboxykinase [GTP]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Corynebacterineae, Mycobacteriaceae, Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- MASS SPECTROMETRY: MW=71209; METHOD=MALDI; RANGE=1-605;
NOTE-Ref.1.
                                                                                                                                                                                                                                                                                                                rnospnoenolpyruvate carboxykinase [GTP] (EC 4.1.1.32) (PEP carboxykinase) (PEPCK).
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; E07A46D4FE35EDC0 CRC64;
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PATHWAY: Rate-limiting gluconeogenic enzyme.
SUBUNIT: Monomer.
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                                                                                                                                                                                                                                 16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Phosphoenolpyruvate carboxykinase [GTP] (EC 4
                                                                                                                                                                                    605 AA.
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Interpro; IPR008210; PEPCK N.
Interpro; IPR008209; PEP_carboxykin.
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                                 227 VRSMQWHSVNVPRDPDCAVCG 247
2 VRSVGWRLQNIGDDMDHAICG 22
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HSSP; P35558; 1KHB.
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                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                         Name=pckG; Synonyms=pck;
Mycobacterium smegmatis
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Best Local Similarity '
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SEQUENCE
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SMART; SM00320; WD40; 2
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Best Local Similarity
9; Conserve
                                                                                       Repeat; WD repeat.
NON TER 1
SEQUENCE 2507 AA;
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A WEDLINE=2198669; PubMed=12210762;

A WEDLINE=2198669; PubMed=12210762;

A WEDLINE=2198669; PubMed=12210762;

A WILLY DE LOZANNE A.;

T Dictyostellum BEACH proteins: phylogenetic and functional analysis of six Dictyostellum BEACH proteins.";

T Dictyostellum BEACH proteins.";

T Dictyostellum BEACH proteins.";

T Dictyostellum BEACH proteins.";

Call. Blacher: 2 WD repeats.

R MILARITY: COntains 2 WD repeats.

R MILARITY: COntains 2 WD repeats.

R InterPro; IPR000409; Beage BEACH.

INTERPRO; IPR000508; Peptidase_226.

INTERPRO; IPR001680; WD40.

R InterPro; IPR01046; WD40.

R Pfam; PF002138; Beach; 1.
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EMBL, CR543861; CAG65571.; -
InterPro; IPR008210; PEPCK N.
InterPro; IPR008210; PEPCK N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                Acinecobacter sp. (strain ADP1).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellacae; Acinecobacter.
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Harris E., Wang N., Wu Wl W.L., Weatherford A., De Lozanne A.,
Cardelli J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.1%; Score 52; DB 2; Length 609; 40.9%; Pred. No. 58; tive 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probom; PD004738; PEPCK_N; 1.
PROSITE; PS00505; PEPCK_GTP; 1.
Complete proteome; Kinage; Lyase; Pyruvate, SEQUENCE proteome; Kinage; Lyase; Pyruvate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
                                         05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Phosphoenolpyruvate carboxykinase (EC 4.1.1.32).
Name=pckG; OrderedLocusNames=ACIAD2842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
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    PRT;
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Mol. Biol. Cell 13:656-669(2002)
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Best Local Similarity 40.99
Matches 9; Conservative
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  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro, IPR008209; PEI
Pfam; PF00821; PEPCK; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                   Length 2507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2929;
                                                                                                                                                                                                                                                                                                                                                                                       Query Match 33.1%; Score 52; DB 2; Length 250 Best Local Similarity 42.9%; Pred. No. 2.5e+02; Matches 9; Conservative 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.1%; Score 52; DB 2; Length 292 llarity 42.9%; Pred: No. 2.96+02. Conservative 4; Mismatches 8; Indels
                                                                                                                                                                                                                                  1 1 2507 AA; 283343 MW; 3821DD88B23CE476 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baumgart C.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0TN-2003 (TrENBLrel. 24, Created)
01-JUN-2003 (TrENBLrel. 24, Last sequence update)
01-MAR-2004 (TrENBLrel. 26, Last annotation update)
Similar to Dictyostellum discoideum (Slime mold). LvsD.
Dictyostellum discoideum (Slime mold). LvsD.
Bukaryota; Mycetozoa; Dictyostellida; Dictyostellum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q851L5 PRELIMINARY; PRT; 417 AA. Q851L5; 01-70N-2003 (TrEMBLrel. 24, Created) 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 2929 AA.
PROSITE; PS50197; BEACH; 1.
PROSITE; PS00501; SPASE I 1; UNKNOWN 1.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1016 WGLPMISEDMDHIISKNSIRI 1036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1438 WGLPMISEDMDHIISKNSIRI 1458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 WRLQNIGDDMDHAICGHDVRL 27
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ij

Gaps

1;

Indels

. 6 2; DB

47;

606 AA.

Length 417;

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Capecanic Faccionsis, STRAIN=H37Rv;

Capecanic Faccionsis, STRAIN=H37Rv;

MEDLINE=98295987; PubMed=9634230; DOI=10.1038/31159;

Cale S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,

A Cale S.T., Brosch S.V., Eiglmedier K., Ghardre C.B. III,

Tekaia F., Badcock K., Bashm D., Brown D., Chillingworth T.,

A Connor R., Davies R.M., Devlin K., Fellwell T., Gentles S., Hamlin N.,

A Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,

Murphy L.D., Oliver S., Seeger K., Skelton S., Squares S., Squares J.,

Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares T.,

B Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

The Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence...;

Mature 393:537-544(1998)...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES—M. Luberculosis; STRAIN-CDC 1551 / Oshkosh;
MEDLINE=22206494; PubMed=12218036;
MEDLINE=22206494; Alland B., Eisen J.A., Carpenter L., White O., Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H., Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M., Rraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Whole-genome comparison of Mycobacterium tuberculosis clinical and
Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M., Overton II L.L., Teitrin T., Kim M.M., Bera J.J., Jin S.S., Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J., Mite O., Salzberg S.L., Fraser C.M.; M., Suh Mite O., Salzberg S.L., Fraser C.M.; Submitted CJUL-2001 to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=pckg; Synonyms=pckA, pck1;
OrderedLocusNames=Rv0211, MT0221, Mb0217; ORFNames=MTCY08D5.06;
Mycobacterium tuberculosis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium bovis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-LOCT-2004 (Rel. 45, Last annotation update)
Phosphoenolpyruvate carboxykinase [GTP] (EC 4.1.1.32) (PEP carboxykinase) (Phosphoenolpyruvate carboxylase) (PEPCK)
                                                                                                                                                                                                                                                                                    Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases. EMBL, AC092557; AAR88567.1; ... Hydrolase. SEQUENCE 417 AA; 43990 MW; 7F1326A1FB883B54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      32.8%; Score 51.5; 43.5%; Pred. No. 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | | ::: | | || || :: | VEWEFKSLEDGRMHA-CGHDVHV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 VGWRLQNIGDDMDHAICGHDVRL 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                     STRAIN=cv. Nipponbare;
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      laboratory strains.
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                                                                                                                                                                                                                                                                             Buell R.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliophida, Poales, Poaceae;
Ehrhartoideae, Oryzee, Oryza, Oryza sativa.
                                 Putative amidohydrolase.

Name-OSJNBa0042109.29; Symonyms=OSJNBa0096106.2;

Name-OSJNBa0042109.29; Symonyms=OSJNBa0096106.2;

Oryza sativa (japonica cultivar-group).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spernatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M., Overton Il L.L., Tsittin T., Kim M., Bera J.J., Jin S.S., Fadrosh D.W., Tallon L.J., Koh H., Zismann V., Hsiao J., Blur S., Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
                                                                                                                                                                                                                                                   Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M., Overtron Il L.L., Tsiturin T., Kim M.N., Bera J.J., Jin S.S., Fadrosh D.W., Tallon L.J., Koo H., Zismann V. Hsiao J., Sl., Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V., Vanaken S.S., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.V., White O., Salzberg S.L., Fraser C.M.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Buell R.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AC104487; AAO41148.1; -.
EMBL; AC092557; AAR86567.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    417 AA; 43990 MW; 7F1326A1FB883B54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; ACCASOLO GESILS; - GRAMED: OBSILS; - GRAMEDE: OBSILS; - GRO; GO: O016787; F: hydrolase activity; IEA. GO; GO: 0008237; F: metallopsptidase activity; IEA. GO; GO: 0006508; P: proteolysis and peptidolysis; IEA. INTERFOR, IPRO1033; Peptidase_MZO. INTERFORD: IRRO10168; Pept MZOD amidh.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR88567 PRELIMINARY, PRT, 417 AA.
AAR88567;
02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Putative amidohydrolase.
            05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 51.5;
Pred. No. 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99 VEWEFKSLEDGKWHA-CGHDVHV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 43.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Buell R.;
Submitted (FEB-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                              FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                               NCBI_TaxID=39947;
                                                                                                                                                                                                                                 SEQUENCE
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SEQUENCE FROM N.A. SPECIES=M.bovis; STRAIN=AF2122/97;

SEQUENCE FROM N.A. STRAIN=cv. Nipponbare;

RESULT 12 AAR88567

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ProDom; PD004738; PEPCK N; 1.
PROSITE; PS00505; PEPCK GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                          Leproma; ML2624; -.
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                                                                                                                                                                                 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=k10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q73TS2
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MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100; Garnier T., Eighmeier K., Camus J.-C., Medina N., Manscor H., Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.; The complete genome sequence of Mycobacterium bovis."; Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00821; rerch, ...
Probom; PD004738; PEPCK N; 1.
PROSITE; PS00505; PEPCK GTP; 1.
Complete protecome; Decarboxylase; Gluconeogenesis; GTP-binding; Lyase.
                                                                                                                 -!- PULA).
-!- PATHWAY: Rate-limiting gluconeogenic enzyme.
-!- SUBJUIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the phosphoenolpyruvate carboxykinase [GTP]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21128732; PubMed=11234002; DOI=10.1038/35059006; Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honoren N., Garnier T., Churcher C.M., Harris D.E., Mungall K.L., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
6-OCT-2001 (Rel. 40, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Phosphoenolpyruvate carboxyxinase [GTP] (EC 4.1.1.32) (PEP carboxykinase) (Phosphoenolpyruvate carboxyxinase) (Name=pcKg; Synonyms=pcKa; OrderedLocusNames=ML2624;
ORFNames=MLCL622.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.5%; Score 51; DB 1; Length 606; 45.5%; Pred. No. 82; tive 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        By similarity.
; AEE29412E6BCCAE3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corynebacterineae, Mycobacteriaceae, Mycobacterium
NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 609 AA
                                                                                                                                                                                                                                                                                                                                                                                               Tuberculist; Rv0211; -.
HAWAP; MF 00452; -; 1.
InterPro; IPR008210; PEPCK_N.
InterPro; IPR008209; PEP_carboxykin.
Pfam; PF00821; PEPCK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             287 GWRAETLGDDIAWMRFGKDGRL 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 GWRLQNIGDDMDHAICGHDVRL 27
                                                                                                                                                                                                                                                                                                             EMBL; BX842572; CAB07006.1; -.
EMBL; AE006931; AAK44442.1; -.
EMBL; BX248334; CAD93081.1; -.
PIR; A70956; A70960.
HSSP; P35558; 1XHB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  606 AA; 67253 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 45.5:
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                              family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MYCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT SITE
SEQUENCE
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PPCK_MYCLE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EVBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L.D., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Ruther. S., Seeger K., Simon S., Simonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R., Barrell B.G., Moodward J.R., Massive gene decay in the leprosy bacillus.";

Nature 408:1107-1011(2001).

-! - CATALYTIC ACTIVITY: GTP + oxaloacetate = GDP + phosphoenolpyruvate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00821; PEPCK; 1.

ProDom; PD00473; PEPCK N; 1.

COMPLETE PS00505; PEPCK TGTP; 1.

ACT SITE 273

ACT SITE

EQUENCE 609 AA; 67731 MM; 891686733622590B CRC64;
                                                                                                                                                                                                                                                                                                                                                      -1- PATHWAY: Rate-limiting gluconeogenic enzyme.
-1- SUBDNIT: Monomer (By similarity).
-1- SUBCELLULA: LOCATION: (Cytoplasmic (By similarity).
-1- SIMILARITY: Belongs to the phosphoenolpyruvate carboxykinase [GTP]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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EMBL; AB017240; AAS06196.1; -.
InterPro; IPR008210; PEPCK N.
InterPro; IPR008209; PEP_Carboxykin.
PF00821; PEPCK; 1.
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Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 32.5%; Score 51; DB 1; Length 609; Best Local Similarity 45.5%; Pred. No. 82; Matches 10; Conservative 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterineae; Mycobacteriaceae; Mycobacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        609 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAMAP; MF 00452; -; 1.
InterPro; IPR008210; PEPCK N.
InterPro; IPR008209; PEP_carboxykin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, 295398; CAB08805.1; -. EMBL, AL583926; CAC32156.1; -PIR, F87237; F87237. HSSP, P35558; IKHB.
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XW Complete proteome.
SQ SEQUENCE 609 AA; 67659 MW; BABF04BFFF2D1847 CRC64;
Query Match
Best Local Similarity 45.5%; Pred. No. 82;
Matches 10; Conservative 3; Mismatches 9; Indels 0; Gaps
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; 0

> Search completed: November 10, 2004, 15:53:22 Job time : 49.0093 secs

6 GWRLQNIGDDMDHAICGHDVRL 27 | | | | | | | | 287 GWRAETLGDDIAWNRFGKDGRL 308

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RESULT 2
US-07-906-930E-33
 oldsymbol{n} and oldsymbol{n} and oldsymbol{n} and oldsymbol{n} and oldsymbol{n} and oldsymbol{n}
Sequence 23033, A Sequence 33, Appl Sequence 24530, A Sequence 24968, A Sequence 21589, A Sequence 21589, A Sequence 21589, A Sequence 21936, A Sequence 20121, A Sequence 2, Appl Sequence 42, Appl
                                                                           November 10, 2004, 14:55:47; Search time 6.01424 Seconds (without alignments) 143.349 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                  Issued_Patents AA:*
1: /csgT2_6/ptodata1/iaa/5A_COMB.pep:*
2: /csgT2_6/ptodata1/iaa/5B_COMB.pep:*
3: /csgT2_6/ptodata1/iaa/6A_COMB.pep:*
4: /csgT2_6/ptodata1/iaa/6B_COMB.pep:*
5: /csgT2_6/ptodata1/iaa/PCTUS_COMB.pep:*
6: /csgT2_6/ptodata1/iaa/PCTUS_COMB.pep:*
            GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-07-906-930B-33
US-09-252-991A-26190
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US-09-252-991A-254968
US-09-252-991A-254968
US-09-252-991A-25490
US-09-252-991A-29509
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US-08-44-670-6
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US-08-461-96-42
US-08-461-96-42
US-08-486-397-42
US-09-249-471-42
US-09-249-471-42
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US-09-249-471-42
US-09-249-471-42
US-09-249-471-42
US-09-249-441-42
US-09-249-441-42
                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                        478139 seqs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                       - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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69
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Maximum DB seq length: 2000000000
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Perfect score: (
Sequence:
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                                                                                Run on:
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VS-09-252-991A-23033

VS-09-252-991A-23033

Sequence 23031, Application US/0925291A

Sequence 23031, Application US/0925291A

Sequence 23031, Application US/0925291A

Sequence 23031, Application Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequen
Sequence 42, Appl Sequence 31721, A Sequence 32998, A Sequence 22948, A Sequence 24912, A Sequence 24012, A Sequence 24012, A Sequence 7, Appl Sequence 2, Appl Sequence 2, Appl Sequence 3, Appl Sequence 2, Appl Sequence 2, Appl Sequence 3, Appl Sequence 22, Appl
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Sequence 33, Application US/07906930E

Patent No. 5534631

GENERAL INFORMATION:
APPLICANT: Gaynor, Richard B.
APPLICANT: Li, Ching
TITLE OF INVENTION: PACTOR (ILF)

NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STREET: Texas
COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 60.1%; Score 41.5; DB 4; Length 501; Best Local Similarity 75.0%; Pred. No. 35; Matches 9; Conservative 1; Mismatches 1; Indels
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US-09-252-991A-32998
US-09-252-991A-22384
US-09-252-991A-22384
US-09-252-991A-24901
US-09-252-991A-24906
US-09-252-991A-24906
US-09-252-991A-2496
US-09-252-991A-2496
US-09-173-300-7
US-09-173-300-7
US-08-669-785-4
US-08-669-785-4
US-08-669-785-4
US-08-669-785-4
US-08-669-785-4
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Fri Nov 12 14:55:53 2004

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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US, 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24968
LENGTH: 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENITION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENITION: AERUGANOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT PAPLICATION NUMBER: US,09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PLILING DATE: 1999-02-18
PRIOR PLILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 25490
                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                              55.1%; Score 38; DB 4; Length 153; 60.0%; Pred. No. 43; tive 2; Mismatches 2; Indels
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Pred. No. 46;
1; Mismatches
          PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26199
LENGTH: 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 24968, Application US/09252991A Patent No. 6551795
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                                                                                                                                                                          ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26199
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Best Local Similarity 85.7%;
Matches 6; Conservative
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Best Local Similarity 60...
Best Local 6; Conservative
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                                                                                                                                                      TYPE: PRT
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ASSOCIATION ASSOCIATION OF THE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38; DB 4; Length 65; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/906,930E
FILING DATE: US-UN-1992
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Sertich, Gary J.
REGISTRATION NUMBER: 34,430
REFERENCE/DOCKET NUMBER: 34,430
REFERENCE/DOCKET NUMBER: 10TSD:262/SER
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 33:
EROUBENE 512-418-3000
TELEPHAX: 512-448-3000
TELEPHAX: 512-448-3000
TELEPHAX: 512-448-3000
TELEPHAX: 512-448-3000
TELEPHAX: 512-44-757
TELEX: DEPLICABLE
INFORMATION FOR SEQ ID NO: 33:
EROUBENCE CHARACTERISTICS:
LENGTH: 494 amino acids
TYPE: amino acid
STRANDENSS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) ORGANISM: Drosophila melanogaster US-09-270-767-44530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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US-09-252-991A-26199
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Sequence 19336, Application US/0925291A

Sequence 19336, Application US/0925291A

Sequence 1935, Application US/0925291A

Sequence 1935, Application US/0925291A

Sequence 1935, Application:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER: OF SEQ ID NOS: 33142

LENGTH: 136

LENGTH: 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 29509, Application US/09252991A
| Sequence 29509, Application US/09252991A
| Patent No. 6551795
| GENERAL INFORMATION:
| APPLICANT: Marc J. Rubenfield et al. |
| APPLICANT: Marc J. Rubenfield et al. |
| TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS |
| FILE REFERENCE: 107196.136 |
| CURRENT APPLICATION NUMBER: US 60/074,788 |
| PRIOR APPLICATION NUMBER: US 60/094,190 |
| PRIOR FILING DATE: 1998-02-18 |
| NUMBER OF SEQ ID NOS: 33142 |
| LENGTH: 269 |
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APPLICANT: Gary Breton et. al
TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PUBLIMONIAL FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
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Pred. No. 57;
1; Mismatches 5; Indels
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50.0%; Pred. No. 1.1e+02;
iive 2; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.0
Matches 6; Conservative
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US-09-252-991A-29509
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US-09-489-039A-8597
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                                                                                                                                                                                                                                    Sequence 21585, Application US/09252991A
Sequence 21585, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21585
LENGTH: 619
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| Sequence 5920. Application US/09513999C
| Patcent No. 678361|
| APPLICANT: Dumas Milne Edwards, J.B.
| APPLICANT: Duclert, A. |
| APPLICANT: Duclert, A. |
| APPLICANT: Glordano, J.Y.
| TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. |
| PATCH No. 6783961|
| PATCH NO. 6783961|
| PATCH REPERBUCE: 59.US2.REG |
| CURRENT FILING DATE: 1999-02-24 |
| PRIOR PPLICATION NUMBER: US 60/122,487 |
| PRIOR PPLICATION NUMBER: US 60/122,487 |
| PRIOR PLING DATE: 1999-02-26 |
| NUMBER OF SEQ ID NOS: 36681 |
| SEQ ID NO 5920 |
| LENGTH: 88 |
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Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels
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53.6%; Score 37; DB
Best Local Similarity 85.7%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches
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; OTHER INFORMATION: Xaa=Pro or Thr
US-09-513-999C-5920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                            113 ŘKPŤCSATSŘ 122
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                                                                             4 RKPTCGSSQR 13
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ORGANISM: Homo sapiens
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LQKPTCG 86
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Score 37; DB 5; Length 1299;
Pred. No. 5.1e+02;
4; Mismatches 1; Indels
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Sequence 6, Application US/08744670

GENERAL INFORMATION:

APPLICANT: Bandman, Olga
APPLICANT: BANDRAN, Olga
APPLICANT: BANDRAN, Olga
APPLICANT: Murry, Lynn E.

ITLE OF INVENTION: TUMOR-ASSOCIATED KAZAL INHIBITOR
INMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STREET: CA
COUNTRY: US
COUNTRY: US
COUNTRY: US
COUNTRY: US
CONPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: DISKETC USCOLUTION SYSTEM: DOS
SOCHWADRE: DISKETC USCOLUTION SYSTEM: DOS
          3: Diskette, 3.50 inch, 720 Kb IBM PS/2
                                                                             SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
CURSITATION UNMBER: PCT/US95/08354A
FILING DATE:
CLASSIFCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/272,368
FILING DATE: 8 JULY 1994
ATTCRNEY/AGENT INFORMATION:
NAME: MONBER: 30,480
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-203 PC
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/744,670
FILING DATE: Filed Herewith
PRIOR APPLICATION DUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/ACTION
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NAME: B111ings, Lucy J.
RECISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0:
TELEPHONE: 415-85-0555
TELEPHONE: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                              TELEPANE: (215) 566-8383
TELEFAX: (215) 568-5549
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1299 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.6%;
                                      COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.0
Matches 5; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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489 IKQPTCGSGR 498
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               MEDIUM TYPE:
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PCT-US95-08354A-2
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS FILE OF INVENTION: ARCUGINGSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
SEQ ID NOS: 33142
SEQ ID NOS: 33142
LENGH: 459
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55.6%; Pred. No. 1.5e+02;
tive 4; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Temple University - Of The APPLICANT: Commonwealth System of Higher Education TILLE OF INVENTION: JAK3 PROTEIN TYROSINE TITLE OF INVENTION: JAK3 PROTEIN TYROSINE TITLE OF INVENTION: MINASE AND DNA ENCODING THE SAME NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS: ADDRESSEE: & Monaco, P.C. STREET: Suite 1800, Two Penn Center CITY: Philadelphia STREET: Suite 1800, Two Penn Center CITY: Philadelphia COUNTY: U.S.A. ZIP: 19102
ZIP: 19102
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
CURRENT APPLICATION NUMBER: US/09/489,039A;
CURRENT FILING DATE: 2000-01-27;
PRIOR APPLICATION NUMBER: US 60/117,747;
PRIOR FILING DATE: 1999-01-29;
NUMBER OF SEQ ID NOS: 14342;
SEQ ID NO 8597;
LENGTH: 362;
TYPE: PRT
CREAMINGH: Klebsiella pneumoniae
US-09-489-039A-8597
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Patent No. 6551795
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 55.6
Matches 5; Conservative
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Best Local Similarity 46.2
Matches 6; Conservative
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8 AGLRRPPAGAERR 20
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168 EPTCGATER 176
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NAME/KEY: UNSURE
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Gaps

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US-09-17-15
US-09-17-15
US-09-17-15
US-09-18-05
US-09-18
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                                                                                                                                                                                                                                                                               DB 2; Length 61;
                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                           Query Match
52.9%; Score 36.5; D.
Best Local Similarity. 80.0%; Pred. No. 32;
Matches 8; Conservative 1; Mismatches
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIERARY: OWL
; CLONE: IPST ANGAN
US-08-744-670-6
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; CLONE: IPST ANGAN
US-09-149-933-6
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Search completed: November 10, 2004, 15:57:19

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sequence 332, App Sequence 577, App Sequence 577, App Sequence 577, App Sequence 172364, Sequence 198430, Sequence 198429, Sequence 198429, Sequence 67911, A Sequence 20990, Sequence 20990, Sequence 219968, Sequence 218927, Sequence 264718, Sequence 264718, Sequence 264718, Sequence 264718, Sequence 64, App Sequence 514, App Sequence 64, App Sequence 518027, Sequence 518027, Sequence 518027, Sequence 518027, Sequence 518027, Sequence 518027, Sequence 518027, Sequence 518027, Sequence 518027, Sequence 518027, Sequence 518027, Sequence 518027, Sequence 518027, Sequence 518027,

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Length 13;
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1 Sequence 65, Application US/10092750

2 Sequence 65, Application US/10092750

3 Sequence 65, Application US/10092750

3 Publication No. US20030032157A1

4 Application No. US20030032157A1

4 Application No. US20030036000

5 TILE REFERENCE: 50036/05002

7 TILE OF INVENTION: Polypeptides Interactive with BCL-X1

7 TILE OF INVENTION WUMBER: US/10/092,750

7 CURRENT FILING DATE: 2002-03-07

7 PRIOR PILING DATE: 2001-03-08

7 NUMBER OF SEQ ID NOS: 253

7 SOFTWARE: BESSEQ for Windows Version 4.0

7 LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
6 US-10-408-765A-1557
3 US-10-707-805-332
3 US-10-707-805-377
4 US-10-707-6622-577
4 US-10-708-846-577
5 US-10-708-846-577
6 US-10-428-115-198429
7 US-10-428-115-198429
7 US-10-428-115-198428
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7 US-10-428-115-219968
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100.0%; Score 69; DB 14;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 13; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 2
US-10-437-963-138965
US-10-437-963-138965
Sequence 138965, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
      ; ORGANISM: Hom
US-10-092-750-65
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Sequence 138965,
Sequence 300236,
Sequence 109125,
Sequence 312228,
Sequence 318616,
Sequence 161045,
Sequence 158860,
Sequence 256799,
Sequence 256799,
                                                                                                                                    November 11, 2004, 02:43:24; Search time 31.4128 Seconds (without alignments) 146.426 Million cell updates/sec
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Sequence
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Published Applications Asia.

1 (902_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

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                          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-437-963-138965
US-10-437-963-109125
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US-10-427-115-318212
US-10-425-115-3182128
US-10-425-115-318616
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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69
1 SGLRKPTCGSSQR 13
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Maximum DB seq length: 200000000
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Match Length DB
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Database :

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Sequence:

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Result

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APPLICANT: La Rosa, Thomas J.
APPLICANT: Exercised to Pavid K.
APPLICANT: Shou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Wi, Wei
APPLICANT: Baukharov, Andrey A.
APPLICANT: Baukharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5321)
CURRENT APPLICATION NUMBER: US/10/437,963
UURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 138962
                                                         APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 109125
LENGTH: 323
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OTHER INFORMATION: Clone ID: PAT_MRI4530_40300C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , OTHER INFORMATION: Clone ID: PAT_MRT4530_13312C.1.pep
US-10-437-963-109125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 61.5%; Pred. No. 1.7e+02;
Matches 8; Conservative 1; Mismatches 4
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Pred. No. 3.2e+02;
1; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEX: unsure
NAME/KEX: unsure
(1)..(323)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-437-963-138962
; Sequence 138962.
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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Best Local Similarity 58.3
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Oryza sativa
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                                           ....rulCANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION UNMBER: US/10/437,963
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 138965
TAND: THING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
THING DATE: 204966
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Publication No. US20040214272A1
Sequence 300236, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Each, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Shou, Y
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71.0%; Score 49; DB 16; Length 95;
Best Local Similarity 66.7%; Pred. No. 2.9;
Matches 8; Conservative 1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: PAT_MRT4530_40303C.1.pep
US-10-437-963-138965
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; OTHER INFORMATION: Clone ID: MRT4577_36886C.1.pep
US-10-425-115-300236
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Pred. No. 16;
0; Mismatches 5
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
La Rosa, Thomas J.
Kovalic, David K.
Zhou, Yihua
Cao, Yongwei
Wu, Wei
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Best Local Similarity 61.5%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Zea mays
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US-10-425-115-300236
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US-10-437-963-109125
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement; FILE REFERENCE: 38-21(53221)B; CURRENT APPLICATION WUMBER: US/10/437,963; CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 161045
LENDING: 137
TYPE: PDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 42564, Application US/10425114
; Sequence 42564, Application US/10425114
; Publication No. US20040034888A1
; Publication No. US20040034888A1
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Soreen, Serven E
; APPLICANT: Gao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 45264
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APPLICANT: Exposite, David K.
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB 16; Length 137;
Pred. No. 1.1e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: PAT_MRT4530_60266C.1.pep
US-10-437-963-161045
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OTHER INFORMATION: Clone ID: 701181349_FLI.pep
US-10-425-114-45264
                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (1)..(137)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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; Sequence 198860, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
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Best Local Similarity 58.3%;
Matches 7; Conservative
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87 SGSRTPSCGAS 97
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                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: unsure
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Sequence 338616, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: AROSA, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

TITLE OF UNENTION: Plants

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

LENGTH: 103
us-l(

"""LIGANT: Zhou, Yihua;

"APPLICANT: Cao, Yongwei;

"TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With;

"TITLE OF INVENTION: Plants;

"TITLE OF INVENTION: Plants;

"TITLE OF INVENTION: NUMBER: US/10/425,115;

"CURRENT APPLICATION NUMBER: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NOS: 369326

LENGTH: 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40; DB 17; Length 90;
Pred. No. 77;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    ; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_47809C.1.pep
US-10-425-115-312228
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US-10-425-115-338616
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LOCATION: (1)..(103)
CHER INFORMATION: unsure at all Xaa locations
PEATURE:
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Publication No. US20040123343A1
GENERAL INFORMATION
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovallc, David K.
APPLICANT: Cao, Yohwa
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey'A.
APPLICANT: Boukharov, Andrey'A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 66.7%;
Matches 8; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GLRKPTCGSSQR 13
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55 GLRRPSCG 62
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Zea mays
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US-10-437-963-161045
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                                                                                                                                                                                                                                           Score 40; DB 16; Length 73
Pred. No. 5.2e+02;
4; Mismatches 2; Indels
                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: PAT_MRT4530_24C.1.pep
US-10-437-963-122034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: RREA, RYCTARO
APPLICANT: RREA, RYCTARO
APPLICANT: TAMBCHIKA, ICHIRO
APPLICANT: YOSHIKANA, TSUTOMU
APPLICANT: YOSHIKANA, TSUTOMU
APPLICANT: YOSHIKANA, TSUTOMU
APPLICANT: MAGAHARI, KENJI
APPLICANT: MAGAHARI, KENJI
APPLICANT: MAGAHARI, KENJI
APPLICANT: MAGAHARI, CRIJI
APPLICANT: MAGAHARI, CRIJI
APPLICANT: MAGAHARI, CRIJI
APPLICANTON NOVEL FULL-LENGTH CDNA
ITILE OF INVERNION: NOVEL FULL-LENGTH CDNA
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PATENTIN VEY: 2.1
SOFTWARE: PATENTIN VEY: 2.1
SOFTWARE: PATENTIN VEY: 2.1
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CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OS SEQ ID NOS: 204966
SEQ ID NO 122034
LENGTH: 734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUGIYAMA, TOMOYASU
OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YUKI
                                                                                                                                                                                                                                               58.0%;
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Best Local Similarity 53.8-
Conservative
                                                                                                                                                                                                                                                                                                                                      1 SGLRKPTCGSSQR 13
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Matches 8; Conservative
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NAGAI, KEIICHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ISOGAI, TAKAO
                                                                                                               TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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US-10-408-765A-1557
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US-10-425-115-256799
; Sequence 256799, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Acvalic, David K.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21 (53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT PILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 226799
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
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                                                                                                                                                                                                                                                                       Length 291;
                                                                                                                                                                                                                                               Score 40; DB 17; Length 25. Pred. No. 2.28+02;
                                                                                                                                                                            FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_112937C.1.pep
US-10-425-115-198860
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, OTHER INFORMATION: Clone ID: MRT4577_16578C.1.pep
US-10-425-115-256799
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LOCATION: (1)..(383)
OTHER INFORMATION: unsure at all Xaa locations
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US-10-437-963-122034
Sequence 122034, Application US/10437963
Publication No. US20040123343A1
GENERAL INPORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Butkharov, Andrey A.
APPLICANT: Butkharov, Andrey A.
PAPLICANT: Panadalk, Brad
  FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 198860
LENGTH: 291
                                                                                                                                                                                                                                                                    58.0%;
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Best Local Similarity 63.6
Matches 7; Conservative
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                                                                                                                                         TYPE: PRT
ORGANISM: Zea mays
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                                                                                          58.0%; Score 40; DB 14; Length 1225; 87.5%; Pred. No. 8.3e+02;
                                                                                                                                              0; Mismatches
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                                                                                             Query Match
Best Local Similarity 87.5
Matches 7; Conservative
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-293-332
                                                                                                                                                                                                                                            615 GLLKPTCG 622
                                                                                                                                                                                             2 GLRKPTCG 9
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APPLICANT: Sahin, Aysegul
APPLICANT: Sahin, Aysegul
APPLICANT: Sahin, Aysegul
APPLICANT: Mills, Gordon B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
FILE REFERENCE: MI-038
CURRENT APPLICATION NUMBER: US 60/299,887
PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR APPLICATION NUMBER: US 60/301,572
PRIOR APPLICATION NUMBER: US 60/305,501
PRIOR FILING DATE: 2001-06-27
PRIOR PILING DATE: 2001-06-27
PRIOR PILING DATE: 2001-07-05
PRIOR PLING DATE: 2001-07-05
PRIOR PLING DATE: 2001-09-25
PRIOR PLING DATE: 2002-03-05
PRIOR PLING DATE: 2002-03-05
PRIOR PLING DATE: 2002-03-05
PRIOR PLING DATE: 2002-03-05
PRIOR PLING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 506
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 332
LENGTH: 1225
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                                      APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: DIBENTIFED IN THE MITOCHONDRIAL PROTEOME
FILE REPERRENCE: 660088 465
CURRENT PAPLICALION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SEQ ID NO 1557
LENGTH: 1011
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Best Local Similarity 87.5%; Pred. No. 7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels (
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Publication No. US20030124128A1
GENERAL INFORMATION:
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Mang, Youtzhen
Xu, Yongyao
Hoersch, Sebastian
Monahan, John
Meyers, Rachel E.
Bast Jr., Robert C.
Hortobagyi, Gabriel N.
Pusztai, Lajos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lillie, James
APPLICANT: Glatt, Karen
APPLICANT: Zhao, Xumen
APPLICANT: Gannavarpu, Manjula
APPLICANT: Kamatkar, Shubhangl
  Soumitra S.
Eoin D.
                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1557
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November 10, 2004, 14:52:32; Search time 4.44128 Seconds (without alignments) 281.634 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                           283416 segs, 96216763 residues
                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                              US-10-092-750-65
69
1 SGLRKPTCGSSQR 13
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Perfect score:
Sequence:
                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                     Run on:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR 79:\*
1: Dir1:\*
2: Dir2:\*
3: Dir3:\*
4: Dir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		hypothetical prote		probable DNA-bindi	interleukin enhanc	·	占	_	Н	hypothetical prote	ATP-	probable aminotran	cal	hypothetical prote	_	ä	_	hypothetical prote	ö	a	ovomucoid (PSTI-ty	hypothetical prote	뉟	Н	Н	Н	hypothetical prote	ս	interleukin-2 rece	hymothetical prote
			T45785	G69369	C85041	B42827	A86266	A41098	T45968	T18316	C72588	G83245	AC0236	T47022	T26453	877401	JC4892	T29315	T24323	158401	TIEEH	G61588	T49831	856310	T16395	H96586	F71111	A87644	C71368	5571	052
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	Score		45.5	43	42	40	40	40	39	39	38	38	38	38	38	37	37	37		37	36.5		36	36	36	36	36	36	36	36	36
	Result No.	; ;	1	N	m	4	Ŋ	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote	dihydroorotase (EC	hypothetical prote	dihydroxy-acid deh	probable VP1/ABI3	DNA topoisomerase	DNA-binding protei	protein C43E11.3 [	adenylate cyclase	cyclolysin - Borde	hypothetical prote	hypothetical prote	hypothetical prote	QRIS protein - yea	mannose-6-phosphat	mob protein B - Er
T49439	AC3412	E84213	S55205	G84708	B87553	QQBE47	B87754	S51672	OYBRC	D96581	F70080	AF3364	S25343	AB2373	JC4728
7	N	N	N	0	N	٦	(7)	N	Н	7	N	N	N	N	N
447	478	559	585	780	899	1128	1590	1705	1706	162	213	80	111	135	161
52.2	52.2	52.2	52.2	52.2	52.2	52.2	52.2	52.2	52.2	51.4	51.4	50.7	50.7	50.7	50.7
36	36	36	36	36	36	36	36	36	36	35.5	35.5	35	35	35	35
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

283416

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

	TASOUR: 1  TASOUR: 1
	Query Match 65.9%; Score 45.5; DB 2; Length 438; Best Local Similarity 83.3%; Pred. No. 3.3; Matches 10; Conservative 1; Mismatches 0; Indels 1; Gaps 1; Qy 1 SGLRKPTGGSQ 12 Db 354 SGLRKP-CGSSE 364
,	RESULT 2  G69369  branched-chain amino acid ABC transporter, ATP-binding protein (braf-3) homolog - Archa (Sybedes: Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004 C;Accession: G69369 K;Klenk, H.D.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodsc.; Fleischmann, R.D.; Quackenbush, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodsc.; Fleischmann, R.D.; Quackenbush, J.F.; White, O.; Nelson, J.F.; McDonald, L. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. MyAuthors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S Smith, H.O.; Woese, C.R.; Venter, J.C. Smith, H.O.; Woese, C.R.; Venter, J.C. A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S Smith, H.O.; Woese, C.R.; Venter, J.C. A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S Smith, H.O.; Woese, C.R.; Venter, J.C. A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S A;Accession: G69369 A;Accession: G6936

Khaykin, E.; Kim, C Maiti, R.; Marziali

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Gaps

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hypothetical protein F7J8.260 - Arabidopsis thaliana (5Species: Arabidopsis thaliana (mouse-ear cress) (5Species: Arabidopsis thaliana (mouse-ear cress) (5Species: Arabidopsis thaliana (mouse-ear cress) (5Species: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004 (5.Date: 04-Feb-2000 #sequence Datebase, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Lessubmitted to the Protein Sequence Database, January 2000 A;Reference number: 223018 A;Reference number: 223018 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-816 <STO>
A;Cross-references: UNIPROT:Q9SAFO; GB:AE005172; NID:g4850400; PIDN:AAD31070.1; GSPDB:Gi
C;Genetics:
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 09-Jul-2004
C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 09-Jul-2004
C;Accession: A41099, A35901
R;Starr, T.V.B.; Prystay, W.; Snutch, T.P.
Proc. Natl. Acad. Sci. U.S.A. 88, 5621-5625, 1991
A;Reference number: A41098; MUID:91288516; PMID:1648226
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A;Residues: 1-2212 (STA>
A;Residues: 1-2212 (STA>
A;Cross-references: UNIPROT:P54282; GB:M64373; NID:g203110; PIDN:AAA40806.1; PID:g203111
A;Cross-references: UNIPROT:P54282; GB:M64373; NID:g203110; PIDN:AAA40806.1; PID:g203111
R;Snutch, T.P.; Leonard, J.P.; Gilbert, M.M.; Leeter, H.A.; Davidson, N.
Proc. Natl. Acad. Sci. U.S.A. 87, 331-3395, 1990
A;Title: Rat brain expresses a heterogeneous family of calcium channels.
A;Reference number: A35901; MUID:90239020; PMID:1692134
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Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

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C.A.; Li, J.H.; Li, Y.; Lin, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.Authors Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M. Wu, D.; Yu, G.; Fraser, C.M.; Vencer, J.C.; Davis, R.W.
A.; Lie: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A. Reference number: A86141; MUID:21016719; PMID:11130712
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C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Superfamily: oxysterol-binding protein; pleckstrin repeat homology
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63.6%; Pred. No. 49;
ive 2; Mismatches 2; Indels
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Pred. No. 1.1e+02;
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1726 SGIQKPECGN 1735
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153 IRKASCGSSNR 163
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A; Residues: 1435-1667 <SNU>
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C; Sunerfamilu
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Matches 7
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C.Species: Homo sapiens (man)
C.Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 12-Sep-1997
C.Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 12-Sep-1997
C.Accession: B42827
C.; Lusis, A.J.; Sparkes, R.; Nirula, A.; Gaynor, R.
Genomics 13, 665-671, 1992
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A;Itle: Characterization and chromosomal mapping of the gene encoding the cellular DNA
A;Reference number: A42827; MUID:92347863; PMID:1339390
A;Accession: B42827
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: A86266
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable DNA-binding protein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Peb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Date: 16-Peb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Date: 16-Peb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
R;Anonymous, The Buropean Union Arabidopsis Genome Sequencing Consortium, The Cold Sprir Nature 402, 76-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: C85041
A;Accession: C85041
A;Accession: C85041
A;Accession: C85041
A;Accession: Teferences: UNIPROT:Q9ZR06; GB:NC_001268; NID:g7270195; PIDN:CAB77810.1; GSPDB:CC;Genetics:
C;Genetics: A;Genetics: A;Amap position: 4
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Pred. No. 33;
1; Mismatches 2; Indels
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Pred. No. 14;
5; Mismatches
                                                                                                   Pred. No. 5;
1; Mismatches
                                                                       Score 43;
Pred. No.
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                                                                   Query Match 62.3%;
Best Local Similarity 77.8%;
Matches 7; Conservative
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53.8%;
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Best Local Similarity 70.0
Matches 7; Conservative
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Best Local Similarity 53.8
Matches 7; Conservative
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probable ATP-binding component of ABC transporter PA3212 [imported] - Pseudomonas aeruginosa (Species: Pseudomonas aeruginosa (Space) (Species: Pseudomonas aeruginosa (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space) (Space)
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C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: ACO236
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.F.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
Nature 413, 523-527, 2001
A;Reference number: AB0001; MUD:21470413; PMID:11586360
A;Reference number: AB0001; MUD:21470413; PMID:11586360
A;Status: preliminary
A;Status: DNA
A;Date: D
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C;Species: Yersinia pestis
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 09-Jul-2004
C;Accession: T47022
R;Buchristesr, C; Rusnick, C; Couve, E; Frangeul, L.; Billault, A.; Kunst, F.; Carnic submitted to the EMBL Data Library, October 1998
A;Description: DNA sequence of the 102 kbases unstable region of Yersinia pestis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q9HZ28; GB:AE004744; GB:AE004091; NID:g9949317; PIDN:AAG066
A;Experimental source: strain PAO1
C;Genetics:
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A,Cross.references: UNIPROT:Q9ZC46; GB:AL590842; PIDN:CAC90751.1; PID:g15979953; GSPDB:
C,Genetics:
A,Gene: YPO1936
C,Superfamily: Escherichia coli valine-pyruvate transaminase
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Pred. No. 59;
0; Mismatches 3; Indels
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Pred. No. 43;
1; Mismatches
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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Best Local Similarity 77.8%;
Matches 7; Conservative
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Best Local Similarity 70.0%;
Matches 7; Conservative (
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57 GLRRPTSGS 65
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C;Species: Leishmania major
C;Species: Leishmania major
C;Accession: T18316
R;Oliver, K.; Murphy, L.; Quail, M.; Lawson, D.; Harris, D.; Rajandream, M.; Ivens, A.;
R;Oliver, K.; Murphy, L.; Quail, M.; Lawson, D.; Harris, D.; Rajandream, M.; Ivens, A.;
R;Oliver, K.; Murphy, L.; Quail, M.; Lawson, D.; Harris, D.; Rajandream, M.; Ivens, A.;
R;Oliver, K.; Murphy, L.; Quail, M.; Lawson, D.; Harris, D.; Rajandream, M.; Ivens, A.;
A;Reference number: Z18876
A;Recession: T18316
A;Recession: T18316
A;Residues: DNA
A;Residues: 1-599 < CLI>A;Residues: 1-599 < CLI>A;Residues: L599 < CLI>A;Residues: L590 < CLI>A;Residues: L590 < CLI>A;Residues: L590 < CLI>A;Residues: L590 < CLI>A;Residues: L590 < CLI>A;Residues: L590 < CLI>A;Residues: L500 < CLI>A;Residues: L
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C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: C72588
R;Kawarabayasi, Y; Hino, Y; Horikawa, H.; Yamazaki, S; Haikawa, Y; Jin-no, K.; Takah Awa, H; Takamiya, M; Masuda, S; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Jun-no, K.; Takah A;Reference number: A1999 #sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A;Reference number: A72450; MUD: 99310339; PMID: 10382966
A;Status: preliminary
A;Molecule type: DNA
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A, Residues: 1-109 < KAW>
A, Cross-references: UNIPROT: Q9YCT6; DDBJ: AP000061; NID: G5104821; PIDN: BAA80161.1; PID: d1
A, Experimental source: strain K1
C, Genetics:
A, Gene: APE1176
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A;Molecule type: DNA
A;Residues: 1-460 <BEV.
A;Crossidues: 1-460 <BEV.
A;Crossidues: UNIPROT:09LFA8; EMBL:AL137189
A;Crossiduental source: cultivar Columbia; BAC clone F7J8
C;Genetics:
A;Map position: 5
A;Introns: 28/2; 57/3; 398/3
A;Note: F7J8.260
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Pred. No. 46;
3; Mismatches
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Pred. No. 56;
2; Mismatches
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Pred. No. 21;
3; Mismatches
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Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||:|:|:| | 80 SGIRRPSSSSSSR 92
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Best Local Similarity 66.7
Matches 6; Conservative
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63 TGLRRPQCG 71
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Best Local Similarity
Matches 7; Conserv
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Search completed: November 10, 2004, 15:55:03
Job time : 5.44128 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein ZC15.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Tact-1999 #sequence_revision 15-Oct-1999 #text_change 09-Ju1-2004
C;Accession: T26453; T27501
R;Lennard, N.
R;Lennard, N.
R;Lennard, N.
R;Lennard, N.
R;Leferon to the EMBL Data Library, November 1998
A;Reference number: Z20216
A;Reference number: Z20216
A;Residues: 1-619 <WILb
A;Rocession: T27601
A;Reference number: C20377
A;Reference number: Z20377
A;Reference number: Z20377
A;Reference number: Z20377
A;Reference number: BEML Data Library, March 1997
A;Reference number: BEML Data Library, March 1997
A;Reference number: Z20377
A;Reference number: Z203
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A;Accession: S77401
A;Accession: S77401
A;Accession: S77401
A;Accession: S77401
A;Accession: S77401
A;Accession: S77401
A;Cross-references: UNIPROT:P73464; EMBL:D90906; GB:AB001339; NID:g1652492; PIDN:BAA1750
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: Synechocystis hypothetical protein s1r1222
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A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: 877401
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda A; T.; Natanabe, A.; Yamada, M.; Yasuda A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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A;Map position: 5
A;Introns: 31/2; 216/3; 279/3; 343/3; 400/3; 428/1; 450/3; 489/1; 532/3; 593/2
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                              A;Cross-references: UNIPROT:092C46; EMBL:AL031866; PIDN:CAA21365.1
A;Experimental source: strain 6/69
C;Superfamily: Escherichia coli valine-pyruvate transaminase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein slr1222 - Synechocystis sp. (strain PCC 6803)
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55.1%; Score 38; DB 2; Length 619;
Best Local Similarity 70.0%; Pred. No. 86;
Matches 7; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                              2; Length 386;
                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                   Score 38; DB
Pred. No. 59;
0; Mismatches
                                                                                                                                                                                                   55.1%;
                                                                                                                                                                517
                                                                                                                                                                                                                                                                                                                                                                                                                                             208 RKPVCASLOR 217
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508 SGMRKPECYS
A;Residues: 1-386 <BUC>
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A.Jouence. Pteriminary
A.Jouence. Pteriminary
A.Residues: 1-376 cQIA-
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A.Residues: 1-376 cQIA-
A.Residues: 1-376 cQIA-
A.Residues: 1-376 cQIA-
A.Cross-references: UNIPROT.028629, GB:U26535, NID:g847787; PIDN:AAA67896.1; PID:g84778
C.Comment: This protein involved in leukocyte-endothelial adhesion; it mediates adhesion
C.Superfamily: L-selectin; C-type lectin homology; complement factor H repeat homology;
F;1-3770main: C-type lectin homology cLCh-
F;29-155/Domain: C-type lectin homology cLCh-
F;360-191/Domain: BGF homology cEGP-
F;197-254/Domain: complement factor H repeat homology <FHI>
F;29-316/Domain: complement factor H repeat homology <FHR>
                                                                                                                                                                                                                                                                                                            L-selectin precursor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004
R;Jatension: J; Huang, X; Marks, R.M.
B;Ochem. B;Ochys. Res. Commun. 225, 406-412, 1996
A;Title: Cloning of the cDNA for rabbit L-selectin and expression of recombinant protein
A;Reference number: JC4892; MUID:96354800; PMID:8753776
A;Status: preliminary
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Pred. No. 85;
2; Mismatches 2; Indels
      2; Length 195;
                                                               Indels
   Score 37; DB
Pred. No. 50;
                                                               Mismatches
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53.6%;
ilarity 54.5%;
Conservative
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Best Local Similarity 60...
      Query Match
Best Local Similarity
Matches 6; Conserv
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streptococc rhodopirell

Q8dyg7 Q8e430

Scoring table:

Searched:

Minimum DB Maximum DB

Database

Result

Perfect score:

Sequence:

OM protein

Run on:

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RT "Complete genome sequence and comparative analysis of the reabclically versatile Pseudomonas putida KT2440.";

metabolically versatile Pseudomonas putida KT2440.";

Environ. Microbiol. 4:799-808(2002).

1- SIMILARITY: Belongs to the ABC transporter family.

BRIS, Po6611 1LTV.

RIGR, P02416. -

CO GO:0005224; F:ATP binding, IEA.

GO: GO:0004009; F:ATP-binding, IEA.

GO: GO:0004009; F:ATP-binding, IEA.

GO: GO:000524; F:ATP-binding, IEA.

CO: GO:000524; F:ATP-binding, IEA.

GO: GO:000525, Roll-binding; IEA.

RICEPPO; IPR003933; AAA ATPase.

InterPro; IPR00393; ABC_transporter.

From: P0000006; ABC_transporter.

From: P0000006; ABC_transporter.

SWART; SM00382; AAA; I.

FROD: BOS0083; ABC_TRANSPORTER. 2; 1.

KW ATP-binding; Complete protecme.

SW SEQUENCE 262 AA; 28148 MW; ABI799A531CD7073 CRC64;
                                         Crurhi rhodopirell
C78918 neurospora
C76652 xenopus lae
C9168 arabidopsis
C97009 leishmania
C67009 leishmania
Aah67016 mus musculu
Aah67016 xenopus lae
C64413 chimpanzee
C99433 cxenopus lae
C64410 xenopus lae
C64410 xenopus lae
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MEDLINE=2423060; PubMed=12534463;
Melon K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
Moazez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  088K75;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last amotation update)
10-MAR-2004 (TrEMBLrel. 26, Last amotation update)
1ron ABC transporter, ATP-binding protein, putative.
0rderedLocusNames=PP2416;
Pseudomonas putida (strain KT2440).
Bacteria; Proteobacteria; Qammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.5%; Score 50; DB 2; Length 262; 75:0%; Pred. No. 1.4; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                262 AA
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                    Q8E430
Q7SURH1
Q7SUR25
Q7NEZ5
Q9DCS2
Q9LFA8
Q9NXL5
AAH67016
Q9W343
Q6W343
Q6W343
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141
88894449226
888944444
748483360
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Query Match
Best Local S:
Matches
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Q88K75
DDAC DDAC BERNAR RANN BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR BERNAR B
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029303 archaeoglob
054728 oryza sativ
054720 oryza sativ
08071 pseudomonas
08071 pseudomonas
08071 macaca fasc
08515 macaca fasc
080431 mus musculu
Aaq17118 mus musculu
Aaq17118 mus musculu
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080430 pseudomonas
0872h3 neurospora
08072h methanosarc
075248 neurospora
0607369 rattus norv
06055 xenopus lae
Aah70855 xenopus lae
Aah70855 xenopus lae
060611 homo sapien
0907368 rattus norv
090611 homo sapien
0907368 rattus norv
090611 homo sapien
0907368 rattus norv
0907368 rattus norv
0907368 rattus norv
090818 rattus norv
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Cae14754 leptospir
Aap82926 ancylosto
O9P084 homo sapien
Q8pgh0 xanthomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arabidopsis
homo sapien
r voltage-d
ancylostoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q88k75 pseudomonas
                                                                                                                                                        November 10, 2004, 14:50:40; Search time 21.79 Seconds (without alignments) 343.270 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                     1825181 segs, 575374646 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
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Q92CZ5
Q92CZ5
Q9CX728
BAD17472
Q9ZK06
Q880R1
Q95K15
Q95K15
Q95K15
Q95K16
Q6WQJ1
AAQ17118
CCHY CAIMO
Q8VMGQ
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                 - protein search, using sw model
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Q872H3
Q8DG19
Q8DG19
Q6NRA8
AAH70855
Q6DU55
Q6DU55
Q5MI1
Q70368
Q9SAF0
Q9SAF0
CCAA RAT
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AAP82926
Q9P084
Q8PGH0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*
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Gapop 10.0 , Gapext
                                                                                                                                                                                                                                                                                                           1 SGLRKPTCGSSOR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq length: 0 seq length: 2000000000
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Match Length
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Gaps

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62.3%;
70.0%;
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Best Local Similarity 7/...
7/. Conservative
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                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                       46 AGLEKPTCG 54
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                                                                                                                                                                                                                                                                               1 SGLRKPTCG
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=39947;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
BAD17472
ID BAD17472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                         Q6YY28;
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Matches
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=VC-16, DSM 4304 / ATCC 49558;

KIENTH-NC-16, DSM 4304 / ATCC 49558;

KIENTH-NC-16, DSM 4304 / ATCC 49558;

KIENTH H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.B.,

KIENTH K.-P., Dodson R.J., Gwinn M.L., Hickey B.K., Peterson J.D.,

Richardson D.L., Kerlavage A.R., Graham D.B., Kyrpides N.C.,

Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.R.,

Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.J.,

Richards B.F., Couthor C.I., Weldman J.F., McDonald L.A.,

Antuterback T.R., Cotton M.D., Sprigge T., Artiach P., Kaine B.P.,

Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujil C.,

Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O.,

Woese C.R., Venter J.C.;

"The complete genome sequence of the hyperthermophilic, sulphate-

Treducing archaeon Archaeoglobus fulgidus.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-07N-1998 (TrEMBLrel. 05, Created)
01-07N-1998 (TrEMBLrel. 05, Last sequence update)
01-07N-1998 (TrEMBLrel. 26, Last annotation update)
01-NR-2004 (TrEMBLrel. 26, Last annotation update)
Branched-chain amino acid ABC transporter, ATP-binding protein (BraF-31) (Methanococus jannasch.
OrderedLocusNames=AF0959;
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                           Enkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                               SEQUENCE FROM N.A.

Belseny W., Berger C., Cooke R., Grellet F., Laudie M., Mewes H.W.,
Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                    ï
                                                                                                                                                                                                                                                                                                                                                                                       65.9%; Score 45.5; DB 2; Length 438; 83.3%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                             EU Arabidopsis sequencing project;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL133452; CAB63018.1; -.
PPR, T45785; T45785.
Hypothetical protein.
SEQUENCE 438 AA; 47254 MW; C0402BID2F43CF0B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Buryarchaeota, Archaeoglobi, Archaeoglobales,
Archaeoglobaceae; Archaeoglobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- SIMILARITY: Belongs to the ABC transporter family.
EMBL, AE001038; AAB90284.1; -.
PIR, G69369; G69369.
                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein F26013.180.
Name=F26013.180;
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212 AA
                                       438 AA
                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    354 SGLRKP-CGSSE 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SGLRKPTCGSSQ 12
                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archaeoglobus fulgidus.
                                                                                                                                                                                                                                                                      [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=2234;
                                                                                                                                                                                   NCBI_TaxID=3702;
                                      Q9SCZ5;
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            RESULT 3
029303
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HISSP, Q58663; 1G9X.

TIGK, AF09595; -.

TIGK, AF09595; -.

ROJ, GO:0016020; C:membrane; IEA.

ROJ, GO:000409; P:ATP-binding; IEA.

ROJ, GO:000409; P:ATP-binding; Cassette (ABC) transporter acti. . .; IEA.

ROJ, GO:000166; F:nucleotide binding; IEA.

ROJ, GO:000166; RABC transporter.

RARRT; SM0382; AAA; I.

RROSITE; PS00211; ABC TRANSPORTER 1; UNKNOWN 1.

RROSITE; PS00211; ABC TRANSPORTER 2; 1.

RATP-binding; Complete protecome.

RATP-binding; Complete protecome.
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10-MAY-2004 (TrEMBLrel. 27, Created)

10-MAY-2004 (TrEMBLrel. 27, Last sequence update)

10-MAY-2004 (TrEMBLrel. 27, Last annotation update)

10-MAY-2004 (TrEMBLrel. 27, Last annotation update)

10-MAY-2004 (TrEMBLrel. 27, Last annotation update)

65.DNBB0056122.17

67.Za sativa (japonica cultivar-group)

67.Za sativa, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

67.Za Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

67.Za Spermatophyta; Cryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sasaki T., Matsumoto T., Katayose Y.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, PAR005644; BAD17472.1; -.
Hypothetical protein.
SEQUENCE 354 AA; 38565 MW; 745AB1B003575BEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein OSJNBb0056122.17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           354 AA
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Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62.3%; Score 43; DB 77.8%; Pred. No. 19;
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Q880R1
Q880R1;
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SEQUENCE FROM N.A.
Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M.,
Spiegel L.A., Huang E.N., Shah R., O'Shaughnessy A., Rodriguez M.,
Preston R.R., Matero A., She L.H., Swaby I., Habermann K., Dedhia N.N.,
Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N.,
Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
105-JUL-2014 (TremBrel. 27, Last annotation update)
106-JUL-2014 (TremBrel. 27, Last annotation update)
107-JUL-2014 (Monse-den 14)
108-JUL-2014 (Monse-den creas)
108-JUL-2014 (Mons
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GO; GO:0005634; C:nucleus; IEA.

GO; GO:0003700; F:transcription factor activity; IEA.

GO; GO:0006355; P:transcription of transcription, DNA-dependent; IEA.

InterPro; IPR001356; Homeobox.

InterPro; IPR009057; Homeodomain_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Habermann K., de la Bastide M., Huang E.N., Gnoj L., Schutz K., Preston R., Calma C., Martienssen R., Parnell L.D., Dedhia N., McCombie W.R.; Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Ciarbelli A.R., Carabelli M., Ruzza V., Sessa G., Steindler C.,
                                                                                                                                                                                                       ö
Length 354;
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Parnell L.D., McCombie W.R.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ruberti I.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parnell L.D.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                / Match 62.3%; Score 43; DB 2; Local Similarity 70.0%; Pred. No. 32; les 7; Conservative 2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                             33 GMRAPSCGSS 42
                                                                                                                                                                                                                                          2 GLRKPTCGSS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=3702;
                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                          Q9ZR06;
                                                                                                                                                                                                                                                                                                                                                                        092R06
                                                                                                                                                                                        Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                     RESULT 6
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RX STRAIN=UCAJOU; PubMed=12228499; DOI=10.1073/pnas.1731982100; RX BUDLINE=22384015; PubMed=12228499; DOI=10.1073/pnas.1731982100; RA BUELINE=22384015; PubMed=12228499; DOI=10.1073/pnas.1731982100; RA BUELINE=223844015; Pulmederg M., Selengut J., Paulsen I.T., Bodson R.J., Dodson R.J., Dosson R.J., Durkin A.S., Kolonay J.F., Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H., RA Nelson W.C., Davidsen T.M., Zafar N., Zhou L., Liu J., Yuan C., A Leterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M., Deng W.-L., Ramos A.R., Afano J.R., Cartinhour S., Chatterjee A.K., Bander C.L., White O., Fraser C.M., Collmer A., Schneider D.J., Tang X., Bender C.L., White O., Fraser C.M., Collmer A., Bender C.L., White O., Fraser C.M., Collmer A., Bender C.L., Mattergae pv. tomato D03000.";

The complete genome sequeme of the Arabidopsis and tomato pathogen Remains Syringae pv. tomato D03000.";

Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186 (2003).

1. SIMILARITY: Belongs to the ABC transporter family.

BRED; ABORGOSSO C: membrane; IEA.

GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.

GO; GO:0004009; F:ATP-binding cassette (ABC)

InterPro; IRR003593; AAA ATPase.

INTERPRO; SWART; SMO0801; ABC Transporter; 2.

REMAIL; SMO0801; ABC Transporter; 2.

REMAIL; SMO0801; ABC Transporter; 2.

REMAIL; SMO0801; ABC Transporter; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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60.9%; Score 42; DB 2; Length 548;
Best Local Similarity 87.5%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                              60.9%; Score 42; DB 2; Length 476; 53.8%; Pred. No. 65; ive 5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM0382; AAA; Z. PROSITE; PS00111; ABC TRANSPORTER 1; 2. PROSITE; PS0893; ABC TRANSPORTER 2; 2. ATP-binding; Complete proteome. SEQUENCE 548 AA; 59616 MW; 38362F8DAB018794 CRC64;
Pfam; PF00046; Homeobox; 1.
PRINTS; PR00024; HOMEOBOX.
SMART; SM00389; HOX; 1.
PROSTITE; PS5071; HOMEOBOX 2; 1.
PROSTITE; PS5071; HOMEOBOX 2; 1.
SMAPT; SM0389; HOMEOBOX 2; 1.
SEQUENCE 476 AA; 53493 MW; D9322A290AFC4F91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
Nickel ABC transporter, ATP-binding protein, putative.
OrderedLocusNames=FSPF03091;
                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 53.0.
Tr Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SGLRKPTCGSSQR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 SGLRQDSCGSTKQ 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=323;
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PRT; 1044 AA.

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CSTBL/6J;
STRAIN=CSTBL/6J;
STRAIN=CSTBL/6J;
Horiquchi S., Taninico K., Takahashi J., Hashimoto N., Nakano I., Teuchida Y., Hirai H., Honjo T.,
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
BMBL, AY275376, AAQ11/Lipase.
InterPro; IPR002921; Lipase.
InterPro; IPR00262; Lipase.
Figur, PP01764; Lipase.
Figur, PP01764; Lipase.
SROULS; Lipase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.4%; Score 41; DB 2; Length 104
70.0%; Pred. No. 2.2e+02;
tive 1; Mismatches 2; Indels
                                                                                                                                        Q6WQJ1,
05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Neural stem cell-derived dendrite regulator.
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Neural stem cell-derived dendrite regulator.
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Best Local Similarity 70.0.
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                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                Name=Nsddr;
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AAQ17118;
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                                                                                                         Q6WQJ1
                                   RESULT 10
Q6WQJ1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NSDDR
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AAQ17118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Costa N., Hida M., Kuenda J., Tanuma R., Hirata M., Suto Y., Hirai M., A Deada N., Hida M., Kuenda J., Tanuma R., Hirata M., Suto Y., Hirai M., Terao K., Sugano S., Hashimoto K.;
Terao K., Sugano S., Hashimoto K.;
Terao K., Sugano S., Hashimoto K.;
Terao K., Sugano S., Hashimoto R.;
Terao K., Sugano S., Hashimoto R.;
Terao K., Sugano S., Hashimoto R.;
Terao K., Subac S., Su
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Brassica napus (Rape).
Brassica napus (Vididiplantae) Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Vididiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Hypothetical protein.
Hypothetical protein.
Hypothetical protein.
Hypothetical protein.
Hypothetical protein.
Hypothetical protein.
Hypothetical protein.
Hypothetical primates; Catarrhini; Cercopithecidae;
Mammalia, Butheria, Primates; Catarrhini; Cercopithecidae;
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STRAIN-Canola;
STRAIN-Canola;
STRAIN-Canola;
Gao Y.P., Gusta L.V.;
Gao Y.P., Gusta L.V.;
Gao Y.P., Gusta L.V.;
Indered (MAR-1999) to the EMEL/GenBank/DDBJ databases.
EMBL; AR139818; AAA38521.1;
InderPro; IPR002628; PSII_MSP.
Pfan; PF01716; MSP; 1.
Pfan; PF01716; MSP; 1.
CRONIENCE 274 AA; 29642 MW; 357A3E62IFF41A0D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05XH68;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
33 kDa oxygen evolving protein of photosystem II.
                                                                          733 AA.
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                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              330 SGLLSPVCGSMQ 341
                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SGLRKPTCGSSQ 12
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                                                                                                                                                                                                                                                                                                                                                                                                          Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      205 RRPTCASSSR 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89HX60
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Q9XH68
RESULT 8
                                   095K15
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Gaps

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Length 1044;

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SEQUENCE FROM N.A.
STRAN=CSPEL/65;
Horiquchi S., Tashiro K., Takahashi J., Hashimoto N., Nakano I.,
Tsuchida Y., Hirai H., Honjo T.; Tsuchida Y., Hirai H., Honjo T.;
Tsuchida Y., Hirai H., Honjo T.;
"NSDDR a novel tetra-spanning transmembrane protein with a unique
integration pattern to the plasma membrane regulates the extension of
the dendritic trees of Purkinje cells.";
Submitted (ARR-2003) to the BMBL/GenBank/DDBJ databases.
ENBL: AY25376; AAQ17118.1; -:
SEQUENCE 1044 AA; 115375 MW; E2AC2349D4B3503E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                            59.4%; Score 41; DB 2; Length 1044; 70.0%; Pred. No. 2.2e+02; ive 1; Mismatches 2; Indels
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RESULT 12 ICHY\_CAIMO

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PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
PROSITE; PS50463; ZN2_CY6_FUNGAL_1; UNKNOWN_1.
PROSITE; PS50048; ZN2_CY6_FUNGAL_2; 1.
DNA-binding; Metal-binding; Nuclear protein; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      German Neurospora genome project;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULA LOCATION: Nuclear (By similarity).
-!- SIMILARITY: Contains 1 Zn(2)-Cys(6) fungal-type binuclear cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; BX224012; CAD70758.1; -.
HSSP; P07248; 2ADR.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005134; C:nucleus; IEA.
GO; GO:0003100; F:transcription factor activity; IEA.
GO; GO:0006357; F:regulation of transcription, DNA-dependent; IEA.
GO; GO:0006357; E:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR007087; Znf C2H2.
Fran; PF000172; Zn C1H2; Z.
Pfam; PF00172; Zn C1H2; Z.
PFNNTS; PR00054; FUNGALZNCYS.
                                                                                                                                                                                                                                                                                                                                                                                                                              Holland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OL-MAR-2001 (TrENBLrel. 16, Created)
01-MAR-2001 (TrENBLrel. 16, Last sequence update)
01-MAR-2004 (TrENBLrel. 26, Last annotation update)
DMRTI protein.
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                 Neurospora crassa.
Eukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                              ъ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 321;
                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B.
Nyakatura G., Mewes H.W., Mannhaupt G.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35330 MW; 91E67B69213E9E9C CRC64;
                                                                                                                                                                                                                       01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40; DB 2;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              325 AA.
                                                                                                                                                                                     321 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
   Pred. No. 36;
0; Mismatches
                                                                                                                                                                                                                                                                             Related to transcriptional activator CMR1
Name=80A10.010;
                                                                                                                                                                                     PRT;
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60.0%;
   77.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00066; GAL4; 1.
SMART; SM00355; ZnF C2H2; 2
   Best Local Similarity 77.8
Matches 7; Conservative
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91 OKPTCGACOK 100
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                                                          2 GLRKPTCGS
                                                                                           18 GLAKPACGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=5141;
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Matches
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                                                                                                                                                                                                                                                                                             "Kazal-type chymotrypsin inhibitor from duck pancreas.";
Comp. Biochem. Physiol. 131B:499-507(2002).
-!-FUNCTION: Inhibits chymotrypsin.
-!-SUBUNIT: Monomer.
-!-SUBCELLULAR LOCATION: Secreted.
-!- MASS SPECTROMETRY: MW=7190.9; MW_ERR=2; METHOD=MALDI; RANGE=1-65;
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MEDLINE=22423065; PubWed=12534468;
Greated A., Lambertson L., Williams P.A., Thomas C.M.;
Grouplete sequence of the IncP-9 TOL plasmid pWW0 from Pseudomonas putida.";
Environ. Microbiol. 4:865-871 (2002).
ENBL; AJ344068; CAC86647.1; --
Hypothetical protein; Plasmid.
SEQUENCE 117 AA; 12700 MW; 22CBA6EEC067638D CRC64;
               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Chymotrypsin inhibitor (DPCI).
Calvina moschata (Muscovy duck).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Cairina.
                                                                                                                                                                                                                       TISSUE-Pancreas;
MEDLINE-21956294; PubMed-11959032;
Wilimowska-Pelc A., Olichwier Z., Mazurkiewicz A., Kowalska J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadaceae, Pseudomonas.
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By similarity.
By similarity.
Reactive bond (By similarity).
360AA7FlAA515D47 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                     SEQUENCE, FUNCTION, SUBUNIT, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
20;
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1- STMILARLTY.

CONTains 1 Kazal-like domain.

HS29, P00995; 1HPT.

InterPro; IPR001339; Prot_inh_Kazal.

InterPro; IPR001339; Prot_inh_Kazal.

FFMEN; PF00050; Kazal; 1.

PRINTS; PR00290; KAZALINHBTR.
     65 AA
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Pred. No. 20;
2; Mismatches
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     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00290; KAZALINHBTR.
SMART; SM00280; KAZAL; 1.
PROSITE; PS00282; KAZAL; 1.
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66.7%;
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   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=303;
ICHY CAIMO
P83039;
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SEQUENCE Query Match

Best Loca Matches

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Q8VMG9 OBVMG9

SO OCC COLORD CO

Query Match

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OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI TaxID=8022;
RN | | 1 | 1 | 1 | 1 | 1 |
RP SEQUENCE FROM N.A.
RA MEDINELS-0435294; PubMed=10978520;
RA Marchand O., Gevoroun M., D'Cotta H., McMeel O., Lareyre J.J.,
RA Marchand O., Gevoroun M., D'Cotta H., McMeel O., Lareyre J.J.,
RA Bernot A., Laudet V., Guiguen Y.;
RA Bernot A., Laudet V., Guiguen Y.;
RA Bernot A., Laudet V., Guiguen Y.;
RY "DARTI expression during gonadal differentiation and spermatogenesis
RT "DARTI expression during gonadal differentiation and spermatogenesis
RY "BREL, AP200955, AG17544.1; -.
DR REMEL, RP200955, AG17544.1; -.
DR REMEL, PR200955, AG17544.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0005635; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0005635; P:regulation of transcription, DNA-dependent; IEA.
DR PRART; SM00310; PM; 1.
DR PAGNITE; PS40000; DM DOMAIN 1; 1.
DR PROSITE; PS40000; DM DOMAIN 1; 1.
DR PROSITE; PS40000; DM DOMAIN 1; 1.
DR PROSITE; PS50809; DM DOMAIN 1; 1.
SQ SEQUENCE 325 AA; 34613 NW; 4FFD2A710F9DF431 CRC64;
Query Match
Best Local Similarity 63.6%; Scote 40; DB 2; Length 325;
Best Local Similarity 63.6%; Scote 40; DB 2; Indels 0; Gaps 0;
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Search completed: November 10, 2004, 15:53:24 Job time: 23.867 secs

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SEQ ID NO 11
LENGTH: 62
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Sequence 12075, A
Sequence 41768, A
Sequence 13449, A
Sequence 36, Appl
Sequence 410, Ap
Sequence 4410, Ap
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                                                                            November 10, 2004, 14:55:47; Search time 11.5658 Seconds (without alignments) 143.349 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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US-09-537-357-11
US-09-537-357-35
US-09-537-357-35
US-09-537-357-35
US-09-537-357-35
US-09-537-355-35
US-09-583-110-2795
US-09-583-110-2795
US-09-583-110-2795
US-09-38-23A-5
US-09-38-23A-5
US-09-38-23A-5
US-09-38-23A-5
US-09-550-876A-6
US-09-550-991A-19103
US-09-252-991A-19103
US-09-252-991A-2463
US-09-252-991A-22648
US-09-252-991A-22648
US-09-252-991A-22648
US-09-252-991A-22648
US-09-252-991A-22648
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US-09-252-991A-219103
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US-09-252-991A-219103
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US-09-252-991A-219103
US-09-252-991A-219103
                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                478139 segs, 66318000 residues
                                                                                                                                               132
1 AGTQPLILAQFMRVGGDELLHFLLW
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext
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| Sequence 27772, Application US/09252991A | Sequence 27772, Application US/09252991A | Sequence 27772, Application US/09252991A | Sequence 27772, Application US/09252991A | Sequence 27772, Application US/09252991A | Sequence 27772, Application: Title OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS | TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS | TITLE OF INVENTION: NUMBER: US/09/252,991A | CURRENT APPLICATION NUMBER: US 60/074,788 | PRIOR PILING DATE: 1998-02-18 | PRIOR PILING DATE: 1998-02-18 | PRIOR PILING DATE: 1998-02-27 | NUMBER OF SEQ ID NOS: 33142 | SEQ ID NO 27772 | LENGTH: 642 |
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Sequence 2, Appli
Sequence 2823, Ap
Sequence 2823, A
Sequence 22239, A
Sequence 21996, A
Sequence 7532, Ap
Sequence 134, App
Sequence 11098, A
Sequence 11064, A
Sequence 11064, A
Sequence 11172, A
Sequence 11865, A
Sequence 31999, A
Sequence 41, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 4955, Ap
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Patent No. 6271018

GENERAL INFORMATION

APPLICANT: Nathalie Tijet

TITLE OF INVENTION: MUSSWALLON (CUCUMIS MELO) HYD

TITLE OF INVENTION: LYASE AND USES THEREOF

FILE REPERENCE: 06027.0002

CURRENT APPLICATION NUMBER: US/09/537,357

CURRENT PILING DATE: 2000-03-29

NUMBER: OF SEQ ID NOS: 56

SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AGTOPLILAQFMRVGGDELLH---FLLW 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Capsicum annum (green pepper)
US-09-537-357-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 42.9
Matches 12, Conservative
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                                                                    Gaps
                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Ian M. Whitehead
APPLICANT: Ian M. Whitehead
APPLICANT: Alan Slusarenko
APPLICANT: Alan Brash
APPLICANT: Alan Brash
TILE OF INVENTION: LYASE AND USES THEREOF
TILE OF INVENTION: LYASE AND USES THEREOF
FILE REFERENCE: 06027,0001
CURRENT FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 25
LENGTH: 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
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; Patent No. 6271018
; GENERAL INFORMATION:
; Alan Brash
; APPLICANT: Alan Brash
; TITLE OF INVENTION: MUSKWELON (CUCUMIS MELO) HYDROPEROXIDE
; TITLE OF INVENTION: LYASE AND USES THEREOF
; FILE REPERENCE: 06022.0002
; CURRENT APPLICATION NUMBER: US/09/537,357
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FASELSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
37.9%; Score 50; DB 3; Length 480;
Best Local Similarity 31.6%; Pred. No. 5.6;
Matches 12; Conservative 5; Mismatches 7; Indels
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                      37.9%; Score 50; DB 3; Length 62; 31.6%; Pred. No. 0.53; 7; Indels ive 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               389 GYQPLVMKDPKVFDEPEKFMLERFTKEKGKELLNYLFW 426
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                                                                                                                                   6 GYQPLVWKDPKVFDEPEKFMLERFTKEKGKELLNYLFW 43
                                                                                                            -LAQFMRVGGDELLHFLLW 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Capsicum annum (green pepper)
US-09-078-173A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Capsicum annum (green pepper)
US-09-537-357-32
                                                                                                                                                                                                                RESULT 3
US-03-078-173A-25
; Sequence 25, Application US/09078173A
; Patent No. 6200794
                          Query Match
Best Local Similarity 31.6
Matches 12, Conservative
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SEQ ID NO 32
LENGTH: 480
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RESULT 5 US-10-042-991-25

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Sequence 2795, Application US/09583110

Facent No. 6699703

GENERAL INFORMATION:
FALL INFORMATION:
FAPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
TITLE OF INVENTION: Number: US/09/583,110
CURRENT APPLICATION NUMBER: US 09/107,433
FRIOR PILING DATE: 1998-06-30
FRIOR PILING DATE: 1998-06-30
FRIOR PILING DATE: 1998-05-12
FRIOR FILING DATE: 1998-05-12
FRIOR FILING DATE: 1998-05-12
FRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
SEQ ID NO 2795
LENGTH: 149
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APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
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Parent No. 6780621
GENERAL INPORMATION:
APPLICANT: Tan M. Whitehead
APPLICANT: Tan M. Whitehead
APPLICANT: Alan Brash
APPLICANT: Alan Brash
APPLICANT: Nathalie Tijet
TITLE OF INVENTION: GUAVA (PSIDIUM GUAJAVA) 13-HYDROPEROXIDE
TITLE OF INVENTION: LYASE AND USES THEREOF
FILE REFERENCE: 06027,0001U3
CURRENT PRILING DATE: 2002-01-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.4%; Score 48; DB 4; Length 149; llarity 53.3%; Pred. No. 3.1; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
37.9%; Score 50; DB 4; Length 480;
Best Local Similarity 31.6%; Pred. No. 5.6;
Matches 12; Conservative 5; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 25
LENGTH: 480
                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT (Green pepper) (Green pepper) 15-10-042-991-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 FMRVGGDELLHFLLW 25
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Best Local Similarity
Matches 8; Conserv
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US-09-583-110-2795
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Gaps
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APPLICANT: Desauvage, Frederic
APPLICANT: Resenthal, Arnon
APPLICANT: Rosenthal, Arnon
APPLICANT: Stone, Donna
ITILE OF INVENTION: Vertebrate Smoothened Proteins
FILE REPERENCE: P1050D1
CURRENT APPLICATION NUMBER: US/09/398,239
CURRENT APPLICATION NUMBER: US/09/398,239
CURRENT FILING DATE: 1999-09-20
EARLIER APPLICATION NUMBER: US 08/720,484
EARLIER FILING DATE: 1996-09-30
NUMBER OF SEQ ID NOS: 5
SEQ ID NO 5
                                     Vertebrate Smoothened Proteins
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COUNTY:
COUNTY:
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COUNTY:
COMPUTER:
CALLECTHICATION
COMPUTER:
MEDIUM TYPE:
3.5 inch, 1.44 Mb floppy disk
COMPUTER:
MEDIUM TYPE:
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MEDIUM TYPE:
COMPUTER:
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Pred. No. 29;
4; Mismatches
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US-06-338-239-5
Sequence 5, Application US/09398239
; Patent No. 6407216
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ORGANISM: Drosophila melanogaster
   APPLICANT: Stone, Donna
TITLE OF INVENTION: Vertebrate
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Matches 10; Conservative
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                                                                                                                                                                                                                                   Score 48; DB 4; Length 219;
Pred. No. 4.8;
                                                                                                                                                                                                                                                                                                         6; Indels
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APPLICANT: Rosenthal, Arnon
APPLICANT: Sosenthal, Arnon
APPLICANT: Stone, Donna
TITLE OF INVENTION: Vertebrate Smoothened Proteins
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSES: Genettech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 138 PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATE:
APPLICATION DATE:
APPLICATION NUMBER: US/08/720,484A
FILING DATE: 30-Sep-1996
CLASSIFICATION: 530
ATTORNAY AGENT INFORMATION:
NAME: SVODGA, Craig G.
REGISTRATION NUMBER: 39-044
REFERENCE/DOCKET NUMBER: 91050
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
36.4%; Score 48; DB
Best Local Similarity 43.5%; Pred. No. 29;
Matches 10; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                      5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-720-484A-5; Sequence 5, Application US/08720484A; Patent No. 5990281; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/08953823A; Sequence 5, Application US/08953823A; Patent No. 613695B; GENERAL INFORMATION:
APPLICANT: Bosauvage, Frederic; APPLICANT: Rosenthal, Arnon
                                                                                                                                                                                                                                                                                                                                                                                                 4 QPLILAQFMRVGGDELLHFL 23
                                                                                                                                                 ORGANISM: Drosophila melanogaster
US-09-270-767-46059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1036 amino acids
                                                                                                                                                                                                                                      36.4%;
Similarity 45.0%;
9; Conservative
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 46059
LENGTH: 219
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TOPOLOGY: Linear
                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 9; Conserv
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TELEFAX: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 36.4%; Score 48; DB 4; Length 1036; Best Local Similarity 43.5%; Pred. No. 29; Matches 10; Conservative 4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/09560876A; Sequence 6, Application US/09560876A; Batter No. 6492139; GENERAL INFORMATION:
APPLICANT: Gauvage, Frederic
APPLICANT: Rosenthal, Arnon
APPLICANT: Stone, Donna; APPLICANT: Stone, Donna; APPLICANT: Stone, Donna; TITLE OF INVERNITON: Vortebrate Smoothened Proteins; FILE REFERENCE: P1050R1D1; CURRENT PILING DATE: 2002-05-22; PRIOR APPLICATION NUMBER: US 60/027,070; PRIOR PILING DATE: 1996-09-30; PRIOR FILING DATE: 1996-09-30; PRIOR FILING DATE: 1997-09-30; NUMBER OF SEQ ID NOS: 6; LENGTH: 1065
           Sequence 5, Application US/09560876A
Patent No. 6423139
GENERAL INPORMATION:
APPLICANT: Beauvage, Frederic
APPLICANT: Rosenthal, Arnon
APPLICANT: Rosenthal, Arnon
TITLE OF INVENTION: Vertebrate Smoothened Proteins
TITLE OF INVENTION: Vertebrate Smoothened Proteins
TITLE OF INVENTION: Vertebrate Smoothened Proteins
FILE REFERENCE: P1050R1D1
CURRENT APPLICATION NUMBER: US/09/560,876A
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: US 60/027,070
PRIOR APPLICATION NUMBER: US 60/027,070
PRIOR APPLICATION NUMBER: US 60/050,000
PRIOR APPLICATION NUMBER: US 60/050,000
PRIOR APPLICATION NUMBER: US 60/051,000
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US-09-560-876A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       788 AGLDPSILNEFLOKNGDFIFPFL 810
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ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Drosophila melanogaster
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NAME/KEY: unsure
LOCATION: 3
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US-09-560-876A-6
-09-560-876A-5
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RESULT 13 US-09-252-991A-18920 ; Sequence 18920, Application US/09252991A

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RESULT 14
US-09-252-991A-19103
is Sequence 19103, Application US/09252991A
is Sequence 19103, Application US/09252991A
is Patent No. 6551795
igeneral information:
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Sequence 26648, Application US/09252991A

Sequence 26648, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: MARC J. Rubenfield et al.

APPLICANT: MARC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPRENCE: 107196.138

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190
APPLICANT: MARC O. Rubenfield et al.
APPLICANT: MARC O. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFREENCE: 107196.136
CURRENT APPLICATION NUMBER: 05 60/074,788
PRIOR APPLICATION NUMBER: 05 60/074,788
PRIOR APPLICATION NUMBER: 05 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
EEGO ID NO 18920
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Pred. No. 21;
1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 ÓPLVAQPRDPLREEAQRORVGGGELOHLAL 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Pseudomonas aeruginosa US-09-252-991A-18920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.8%;
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Best Local Similarity 43.3%;
Matches 13; Conservative
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Best Local Similarity 52.6'
Matches 10; Conservative
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                                                                                                                                                    Query Match 34.8%; Score 46; DB 4; Length 566; Best Local Similarity 55.0%; Pred. No. 31; Matches 11; Conservative 1; Mismatches 8; Indels
                                                                                                                                                                                                                                                       339 LVAAQDERPGADRLLVDLLW 358
                                                                                                                                                                                                                           6 LILAQFMRVGGDELLHFLLW 25
; PRIOR FILING DATE: 1998-07-27; NUMBER OF SEQ ID NOS: 33142; SEQ ID NO 26448; LENGTH: 566; TYPE: PRT ORGANISM: Pseudomonas aeruginosa US-09-252-991A-26648
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Search completed: November 10, 2004, 15:57:20 Job time : 12.5658 secs

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Sequence 214, App Sequence 236063, Sequence 24600, A Sequence 164152, Sequence 164152, Sequence 177358, Sequence 177358, Sequence 144679, Sequence 144680, Sequence 147272, Sequence 147272, Sequence 204013, Sequence 204013, Sequence 219262, Sequence 195460, Sequence 195460, Sequence 195460, Sequence 195460, Sequence 195460, Sequence 195460,

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; Sequence 229512, Application US/10425115; Publication No. US20040214272A1; GENERAL INFORMATION:

RESULT 2 US-10-425-115-229512

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Gaps

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Length 163;

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Page 2

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21 (53313)B

CURRENT APPLICATION NUMBER: 105/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 40985

LENGTH: 163

TYPE: n...
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongweic
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
FILE REFERENCE: 2003-04-28
CURRENT APPLICATION UNDER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/09884260A

Sequence 11, Application US/09884260A

Batent No. US20202098570A1

GENERAL INFORMATION:

APPLICANT: Alan Brash

APPLICANT: Nathalier Tijet

TITLE OF INVENTION: MYSKMELON (CUCUMIS MELO) HYDROPEROXIDE

TITLE OF INVENTION: LYASE AND USES THEREOF

FILE REFERENCE: 06027.000202

CURRENT APPLICATION NUMBER: US/09/884,260A

CURRENT FILING DATE: 2001-06-19

PRIOR PILING DATE: 2000-03-29

NUMBER OF SEQ ID NOS: 56

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GTOPLI ------LAOFMRVGGDELLHFLLW 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: LIB3059-042-B9_FLI.pep
US-10-425-114-40985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
38.6%; Score 51, DB 15,
Best Local Similarity 50.0%; Pred. No. 5.9;
Matches 10; Conservative 5; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) ORGANISM: Capsicum annum (green pepper)
US-09-884-260A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 327061, Application US/10425115 Publication No. US20040214272A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Zea mays
FEATURE:
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US-10-425-115-327061
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US-09-884-260A-11
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     us-10-C

APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Applicant: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Sal-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 229512
LENGTH: 168
TYPE: Thomas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Zhou, Yihua APPLICANT: Zhou, Yihua APPLICANT: Kovalic, David K. APPLICANT: Screen, Seeven E APPLICANT: Screen, Jack E APPLICANT: Tabaska, Jack E APPLICANT: Tabaska, Jack E APPLICANT: Tabaska, Jack E TITLE OF INVENTION: Mucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement TITLE OF INVENTION: PLANTS and Uses Thereof for Plant Improvement CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT PILING DATE: 2003-04-28
SEQ ID NO 48127
LENGTH: 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40.5%; Score 53.5; DB 17; Length 168; 44.0%; Pred. No. 2.4; tive 4; Mismatches 3; Indels 7;
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38.6%; Score 51; DB 15; Length 161;
Best Local Similarity 50.0%; Pred. No. 5.8;
Matches 10; Conservative 5; Mismatches 5; Indels
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US-10-425-114-48127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ), OTHER INFORMATION: Clone ID: MRT4577_140909C.1.pep
US-10-425-115-229512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEX: unsure
COCATION: (1)..(168)
OTHER INFORWATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AGTOPLILAQFMRVGGDELLHFLLW 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
US-10-425-114-40985
US-10-425-114-40985
Sequence 40985, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICAWT: Liu, Jingdong
APPLICAWT: Zhou, Yihua
ROPLICANT: Rovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 48127, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AGTQPLILAQFMRVGGDELL 20
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22 AGLEPLLKARFGRLAGGDLL 41
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Best Local Similarity 44.04
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-425-114-48127
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US-10-155335

Sequence 5535, Application US/10767701

Sequence 5535, Application US/10767701

Sequence 5535, Application US/10767701

Sequence 5535, Application US/10767701

Sequence 5535, Application US/2040172684A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwal

APPLICANT: Cao, Yongwal

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT PILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

LENGTH: 103
                                                                                                                                                                                                                           APPLICANT: INTENDED M. Whitehead
APPLICANT: Alan Slusarenko
APPLICANT: Alan Slusarenko
APPLICANT: Alan Susarenko
APPLICANT: Duncan Gaskin
APPLICANT: Duncan Gaskin
APPLICANT: Mathalie Tijet
TITLE OF INVENTION: GUAVA (FSIDIUM GUAJAVA) 13-HYDROPEROXIDE
TITLE OF INVENTION: GLOST.0001U3
TITLE OF INVENTION: 10027.0001U3
FILE REFERENCE: 06027.0001U3
CURRENT APPLICATION NUMBER: US/10/042,991
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 25
LENGTH: 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 37.9%; Score 50; DB 13; Length 480; Best Local Similarity 31.6%; Pred. No. 28; Matches 12; Conservative 5; Mismatches 7; Indels 1
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Pred. No. 11;
1; Mismatches 8; Indels
     389 GYQPLVMKDPKVFDEPEKFMLBRFTKEKGKELLNYLFW 426
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LOCATION: (1)..(103)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
; OTHER INFORMATION: Clone ID: 30161891.pep
US-10-767-701-55335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Capsicum annum (green pepper)
US-10-042-991-25
                                                                                                       RESULT 9
US-10-042-991-25
US-10-042-991-25
; Sequence 25, Application US/10042991
; Publication No. US20020142407A1
; GENERAL INFORMATION:
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Best Local Similarity 55.0%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
US-10-425-114-53219
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Publication No. US20040088752A1
GENERAL INFORMATION:
APPLICANT: Howe, Gregg
APPLICANT: Howe, Gregg
APPLICANT: Itch, Aya
TITLE OF INVENTION: Divinyl Ether Synthase Gene, Protein, and Uses Thereof
FILE REFERENCE: MSU-06818; US/10/381,870
CURRENT APPLICATION NUMBER: US/10/381,870
PRIOR PELICATION NUMBER: 60/238,415
PRIOR FILING DATE: 2003-11-17
PRIOR FILING DATE: 2000-10-06
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.0
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| Sequence 32, Application US/09884260A
| Patent No. US20020098570A1
| GENERAL INFORMATION:
| APPLICANT: Alan Brash
| APPLICANT: Alan Brash
| TITLE OF INVENTION: MUSKMELON (CUCUMIS MELO) HYDROPEROXIDE
| TITLE OF INVENTION: LYASE AND USES THEREOF
| TITLE OF INVENTION: LYASE AND USES THEREOF
| TITLE OF INVENTION: MUMBER: US/09/884,260A
| CURRENT PILICATION NUMBER: 09/,537,357
| PRIOR APPLICATION NUMBER: 09/,537,357
| PRIOR PILICAN DATE: 2001-06-19
| WINDER OF SEQ ID NOS: 56
| NUMBER OF SEQ ID NOS: 56
| COFFWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 37.9%; Score 50; DB 15; Length 476; Best Local Similarity 31.6%; Pred. No. 28; Matches 12; Conservative 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.9%; Score 50; DB 9; Length 480;
31.6%; Pred. No. 28;
tive 5; Mismatches 7; Indels
                                                                                                                                                                                      Query Match 37.9%; Score 50; DB 17; Length 70; Best Local Similarity 47.1%; Pred. No. 3.4; Matches 8; Conservative 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    385 GYOPLVMKDPKVFDEPEKFVLERFTKEKGKELLNYLFW 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GTQPL-----ILAQFMRVGGDELLHFLLW 25
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                                                                              ; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_6134C.1.pep
US-10-425-115-327061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Capsicum annum (green pepper)
US-09-884-260A-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT / ORGANISM: Lycopersicon esculentum US-10-381-870-5
                                                                                                                                                                                                                                                                                                                                23 ASVQPVLIQQYMSVGGE 39
                                                                                                                                                                                                                                                                                                 1 AGTOPLILAQFMRVGGD 17
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Best Local Similarity 31.63
Matches 12; Conservative
LENGTH: 70
TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GTQPLI-
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LENGIH: 476
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LENGTH: 480
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US-10-381-870-5
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Gaps

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APPLICANT: Shen, Le1
APPLICANT: Shen, Le1
APPLICANT: Shankets, Richard A.
APPLICANT: Shankets, Richard A.
APPLICANT: Spaderna, Steven K.
APPLICANT: Taupier, Bayan J. Jr.
APPLICANT: Taupier, Bryan D.
APPLICANT: Voss, Edward S. Jr.
APLICANT: Voss, Bryan D.
APPLICANT: Voss, Bryan D.
APPLICANT: APPLICATION NUMBER: US/10/190,115
CURRENT FILING DATE: 2001-07-05
PRIOR PLING DATE: 2001-07-05
PRIOR PLING DATE: 2000-07-03
PRIOR PLING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/215,856
PRIOR PLING DATE: 2000-07-03
PRIOR PLING DATE: 2000-07-03
PRIOR PLING DATE: 2000-07-03
PRIOR PLING DATE: 2000-07-03
PRIOR PLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/216,586
PRIOR PLING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/216,586
PRIOR PLING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/216,586
PRIOR PLING DATE: 2000-07-07
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PRIOR APPLICATION NUMBER: 60/216,586
PRIOR APPLICATION NUMBER: 60/216,586
PRIOR PLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/216,586
PRIOR PLING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/216,586
PRIOR PLING DATE: 2000-07-07
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ilarity 54.5%; Pred. No. 3.5e+02;
Conservative 3; Mismatches 5.
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US-10-369-072-28

Sequence 28, Application US/10369072

Publication No. US20040014081A1

GENERAL INFORMATION:

APPLICANT: Spaderna, Stephen K

APPLICANT: Tchernev, Velizar

APPLICANT: Liu, Xiachong

APPLICANT: Shenoy, Suresh
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                                                                                                                                                                                                                   Mezick, Amanda J.
Padigaru, Muralidhara
                                           Casman, Stacie J.
Grosse, William M.
Gusev, Vladimir Y.
Ji, Weizhen
Lepley, Denise M.
Liu, Kiaohong
                                                                                                                                                                                                                                                                        Patturajan, Meera
Rastelli, Luca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                      Shen, Lei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-190-115-28
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APPLICANT:
APPLICANT:
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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: APPLICANT: Ascreen, Serven E
APPLICANT: Cao, Yongwei
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TILE OF INVENTION: Dlants and Uses Thereof for Plant Improvement
TILE OF INVENTION: Dlants and Uses Thereof for Plant Improvement
TILE OF SEQ ID NOS: 73128
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
Sequence 53219, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Liu, Jingdong

APPLICANT: Schou, Yihua

APPLICANT: Schou, Yihua

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Program Cao, Yongwai

ITILE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE SERERENCE: 38-21 (3313) B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

LENGTH: 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 47.1%; Pred. No. 32;
Matches 8; Conservative 5; Mismatches 4: Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) OTHER INFORMATION: Clone ID: LIB3060-081-H7_FLI.pep
US-10-425-114-67552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Clone ID: 700242574_FLI.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 28, Application US/10190115; Publication No. US20030207394A1; GENERAL INFORMATION: APPLICANT: Alsobrook, John P. II; APPLICANT: Boldog, Ferenc L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AGTOPLILAQFMRVGGD 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 AKVQPVLIQQYMSVGGE 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AGTOPLILAOFMRVGGD 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-425-114-53219
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LENGTH: 287
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US-10-190-115-28
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us-10-092-750-66.rapb
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APPLICANT: Explay, bunder o
APPLICANT: Explay, Denise M
APPLICANT: Starkets, Catherine B
APPLICANT: Shinkets, Richard
APPLICANT: Shinkets, Richard
APPLICANT: Shinkets, Richard
APPLICANT: Shinkets, Richard
APPLICANT: Shinkets, Richard
APPLICANT: Shinkets, Richard
APPLICANT: Shinkets, Richard
APPLICANT: Shinkets, Richard
APPLICANT: Shinkets, 100,100,2018

TILES OF INVENTION NUMBER: US/10/369,072
CURRENT FILING DATE: 2003-02-18
PRIOR FILING DATE: 2003-02-18
PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/215,854
PRIOR FILING DATE: 2000-07-03
PRIOR FILING DATE: 2000-07-03
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/216,586
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/216,586
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/216,586
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PRIOR APPLICATION NUMBER: 60/216,586
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PRIOR FILING D
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36.4%; Score 48; DB 15; Length 2447;
Best Local Similarity 54.5%; Pred. No. 3.5e+02;
Matches 12; Conservative 3; Mismatches 5; Indels :
                                        Zerbusen, Bryan
Patturajan, Meera
Taupier, Raymond T
Rastelli, Luca
Grosse, William M
Szerkeres, Edward S
Lepley, Denise M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT; ORGANISM: Takifugu rubripes
US-10-369-072-28
Spytek, Kimberly
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2; Gaps

ð 셤 RESULT 15
US-10-306-762-214

Sequence 214, Application US/10306762

Publication No. US2030187220A1

GENERAL INFORMATION:

APPLICANT: Park, Frances

APPLICANT: Buchana, Sean Grant

APPLICANT: Buchana, Sean Grant

APPLICANT: Buchana, Sean Grant

APPLICANT: Sauder, J. Michael

TILLS OF INVENTION: CRYSTALS AND STRUCTURES OF A FLAVIN

TILLS OF INVENTION: MONONUCLECTIDE BINDING PROTEIN (FUNBP)

TILLS REPREBNOS: 52498-20011.00

CURRENT APPLICATION NUMBER: US/10/306,762

CURRENT FILLING DATE: 2003-04-16

PRIOR APPLICATION NUMBER: US 60/334,132

PRIOR FILLNG DATE: 2001-11-28

NUMBER OF SEQ ID NOS: 242

SEQ ID NO 214

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..
                                                                           Query Match 35.6%; Score 47; DB 14; Length 315; Best Local Similarity 50.0%; Pred. No. 53; Matches 8; Conservative 4; Mismatches 4; Indels
; TYPE: PRT
; ORGANISM: D hafniense (23116726)
US-10-306-762-214
                                                                                                                                                                  2 GTOPLILAGEMRVGGD 17
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62 GSEPALLAQAARIGAD 77
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Search completed: November 11, 2004, 07:41:45 Job time : 60.4093 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

November 10, 2004, 14:50:40 ; Search time 41.9039 Seconds (without alignments) 343.270 Million cell updates/sec Run on:

Title: US-10-092-750-66
Perfect score: 132
Sequence: 1 AGTQPLILAQFMRVGGDELLHFLLW 25

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

1825181 segs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt\_02:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	•	ycobact	vo	H	~	_	~	~	Q93yf8 nicotiana a		_		7	Δ1	O85168 pseudomonas	σı	Q95ss8 drosophila		Q924a5 plasmid col	Q7djm3 plasmid r64	solanum	citrus	C	31 citrus j	Þ	41	18 suberi	Q6glq4 xenopus lae	P91682 drosophila	Q86pa9 drosophila	Ol3149 fugu rubrip
SOUTHERNIES	ID	Q6FK21	Q73YV9	AAS04161	Q9LLA9	Q9ARH8	SOXGIB	Q39443	Q9ARH7	Q93YF8	Q7UUN1	Q868N1	058294	Q27807	065152	085168	Q8CYZ9	095888	Q79VT3	Q9Z4A5	Q7DJM3	Q93X18	Q76LM3	Q84V86	BAC55161	Q70SU0	CAD79441	CAD66418	Q6GLQ4	0	φ	013149
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	Score	51	20	20	20	50	20	20	50	20	49	4.9	49	4 9	49	49	4.8	4.8	48	48	48	48	4.8	48	48	48	48	48	48	48	48	48
	Result No.		73	ო	4	ιΩ	φ	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29		31

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073YV9 PRELIMINARY; PRT; 456 AA. 073YV9; 05-JUL-2004 (TEMBLrel. 27, Created) 05-JUL-2004 (TEMBLrel. 27, Last sequence update)

RESULT 2 Q73YV9 ID Q73YY AC Q73YY DT 05-JI

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Q25542 nereis dive Q8ht81 selaginella Q6bm19 debaryomyce	0,.		Q89wq1 bradyrhizob Q7sie4 thermus the	Q72gm3 thermus the Aas82167 thermus t	Q896q1 clostridium O8zxm2 ovrobaculum	
Q25542 Q8HT81 Q6BML9	Q9RV87 Q88VK1	Q9KUK1 Q8PG03	SYL BRAJA Q7SÎE4	Q72GM3 AAS82167	Q896Q1 Q82XM2	Q7CWZ9
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235 371 409	480 569	625 740	874 878	878 878	457	294
35.6	35.6	35.6 35.6	35.6 35.6	35.6	35.2	34.8
7 4 4 7 7 4	74	7 <del>4</del> 7	47	47	46.5	4.
332	9 B	337	6.4 0.0	4 1 2 2	4. 4 E. 4	4.5

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		í	ate)	SR079c RPG1.				; Candida.					asaregola S.	lise C., Tal	Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe	Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,	Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar	H., Groppi	Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri	Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,	Nicaud J.M., Nikolbki M., Oztas S., Ozier-Kalogeropoulos C.,	sethof E. W	M. Thierry A.	Gaillardin C., Weissenbach								A CRC64;	Length 951;	; Indels
1 A.A.		ed) segmence undate)	annotation update)	sp P38249 Saccharomyces cerevisiae YBR079c		glabrata (Yeast) (Torulopsis glabrata).	Saccharomycotina;	Saccharomycetales;					ns P., C	, Neuveg	louard V.	Beyne E	nfaniole	y-Dumaze	Joyet P	ır I., Ma	er-Kaloge	M G	Fukuhara	Bouchier C., Caudron B., Scarpelli C., Gaillardin C								DC6B47AEBB351A5A	7,	thes 7;
951		ر وورور	nota	cere		s 91	arom	агош					urre	ن بر	Anth	Σ̈́	S,	Ferr	ż	Lesu	CZ	ָרְיָּרְיִּרְיִּרְיִּרְיִּרְיִּרְיִּרְיִּרְיִ	110						Ä.			B47A		
PRT;	•	Created)	Last an	omyces									G., D	., Marc	le M.,	erich J	lico L.	ad C.,	auniaux	e w	נים מיני	owaki -	Bolo	rpelli		·.			_like_DNA.				Score 51;	Fred. NO. 36; 2; Mismatches
Υ,	ļ	. 27,	27.	acchar		t) (To)	Eukaryota; Fungi; Ascomycota;	Saccharomycetales, mitosporic					Fischer	igny J	., Aig.	, Becke	Catto	Fairhe	C.	Lemai	M., Ozt	Meno	04.50	Scal	Ι.,	evolution in yeasts.		99.1;	ambda_	CI.	-	110156 MW;	38.6%;	•• ••
PRELIMINARY		(TrEMBLrel.	(TrEMBLirel, 27,	3249 S	1804g;	(Yeas	; Asco	s; mit		4			, O c	e Mont	geul L	nin S.	er J.,	() (i)	neguin	ן: אין:	OIBK1	ים מינה הים מינה	717.20	dron B	Souciet J.L.;	n in y	430:35-44 (2004)	CAG623	982; L	717; P	PINT;	A; 11		vat
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		2004	12004	r to	BE-CA	a glal	ota; 1	romyc	=CIXE	CE FR	-CBS1.	VURES	B., SI	aine :	, . Z T		ne A.	9 Г.,	ye F	E A.,	٠. ت	, ,	No.	i i	г Р.,	e evo	430:	CR380	10; H	ro;	SMOO	8	i,	
LT 1 21 Q6FK21	Q6FK21;	05-JUL-2004	05-1111-2004	Similar to	ORFNames=CAGLOM01804g;	Candida	Eukary	Sacchai	NCBI Taxid=5478;	SECUENCE FROM N.A.	STRAIN=CBS138;	GENOLEVURES;	Dujon 1	Lafonta	Goffar	Barnay	Boisran	Despon	Hantra	Kerrest	Nicaud	Swenner	Zenion	Bouchie	Wincker P.,	"Genome	Nature	EMBL; CR380959; CAG62399.1;	InterP	InterPro; IPR000717; PCI.	SMART;	SEQUENCE 951 AA; 1	Query Match	Best Local Matches
RESULT Q6FK21 ID Q	AC	E E		田口	NS C	SO	8	8	Š	Z 2	RC	RG	RA	æ	RA	RA	Æ	RA.	RA.	RA.	Z G	5 6	5 0	<b>5</b> 5	Æ	RT	EL	DR.	DR.	N.	ä	SQ	ð	Ма

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Lycopersicon esculentum (Tomato).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids,
Lamids, Solamales, Solamacese, Solanum.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
NCBI_TAXID=4081;
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MbMed=10859201; MBDLINE=20317213; PubMed=10859201; Howe G.A., Lee G.I., Itoh A., Li L., DeRocher A.E.; Howe G.A., Lee G.I., Itoh A., Li L., DeRocher A.E.; and eyfo-dependent metabolism of oxylipins in tomato. Cloning and expression of allene oxide synthase and fatty acid hydroperoxide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Richard S., Atwal A.S.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2001) to the Cytochrome P450 family.
EMBL; ANO28373; AAKZ7265-1; -
PIR; JC7304; JC7304; Jrase activity; IEA.
GO; GO:0016829; F:Hyase activity; IEA.
GO; GO:0004497; F:monooxygenase activity; IEA.
InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR0012403; EP450IV.
PF00067; P450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.9%; Score 50; DB 2; Length 476; 31.6%; Pred. No. 39; 7; Indels ive 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant Physiol. 123:711-724(2000).
-!- SIMILARITY: Belongs to the cytochrome P450 family.
EMBL. AF230372; AAF67142.1; -.
GO: GO:0016829; F:1yase activity; IEA.
GO: GO:0004497; F:moncoxygenase activity; IEA.
GO: GO:000618; P:noncoxygenase activity; IEA.
InterPro; IPR00128; Cytochrome_P450.
InterPro; IPR00128; Cytochrome_P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABOEA80F0C97C4EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        476 AA; 53480 MW; 4A56DDB8131FB1C1 CRC64;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fatty acid hydroperoxide lyase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-UTN-2001 (TrEMBLrel. 17, Created)
01-UTN-2001 (TrEMBLrel. 17, Last sequence update)
01-UTN-2003 (TrEMBLrel. 25, Last annotation update)
Fatty acid hydroperoxide lyase.
Lycopersicon esculentum (Tomato).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            385 GYÓPLVMKDPKVFDEPEKFVLERFTKEKGKÉLLNYLFW 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GTQPL-----ILAQFMRVGGDELLHFLLW 25
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Best Local Similarity 31.6%
....hes 12; Conservative
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PRINTS; PR00465; EP450IV.
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                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4081;
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SEQUENCE 4
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Q9ARH8
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                                                                                                                                                                                                                                                                                                                 Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
-! COFACTOR: FAD (By similarity).
-!- SIMILARITY: Belongs to the class-I pyridine nucleotide-disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AE017233; AASO4161.1; -
SEQUENCE 456 AA; 48736 MW; B36BB27F78C2451E CRC64;
                                                                            Mycobacterium paratuberculosis.

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corprebacterineae; Mycobacterineae; Mycobacterium; Mycobacterium avium complex (MAC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium paratuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1770;
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37.9%; Score 50; DB 2; Length 456;
Best Local Similarity 41.7%; Pred. No. 38;
Matches 10; Conservative 6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 456; 38;
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Oxidoraturis and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and particle and pa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Redox-active center.
SEQUENCE 456 AA; 48736 MW; B36BB27F78C2451E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AASO4161 PRELIMINARY; PRT; 456 AA.
AASO4161;
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 37.9%; Score 50; DB Best Local Similarity 41.7%; Pred. No. 38; Matches 10; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    396 ADTREILGAAILGVGGDEAIHGIL 419
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                                                          Name=1pd; OrderedLocusNames=MAP1844c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AGTOPLILAOFMRVGGDELLHFLL 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AGTOPLILAOFMRVGGDELLHFLL 24
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Matches

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RESULT 3 AAS04161

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Gaps

14;

RESULT 09LLA9

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SEQUENCE FROM N.A.
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                                                                       Heme; Lyase
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                                                                                     SEQUENCE
                                                                                                             Query Match
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                                                                                                                                      Matches
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1. Similarity: Belongs to the cytochrome P450 family.

2. -!- SIMILARITY: Belongs to the cytochrome P450 family.

3. FIR: JG7304, OG7304.

3. FR. JG7304, OG7304.

3. FR. JG7304, OG7304.

3. GO; GO:0016829; F: Monooxygenase activity; IEA.

3. GO; GO:0006189; F: Monooxygenase activity; IEA.

3. GO; GO:0006189; F: Monooxygenase activity; IEA.

3. DR GO; GO:0006189; F: Monooxygenase activity; IEA.

3. DR FIREPRO; IPR001128; Cytochrome_P450.

3. DR FRAM; PR000465; EP450IV.
                                                                                                                                                                                                                     Lycopersicon esculentum (Tomato).
Bukarycota, Viridijalaries, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplatae, Erreptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids,
lamids, Solanales, Solanaceae, Capsicum.
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                         14;
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   Length 476;
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                         7; Indels
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TISSUE-Fruits;
Matsui K., Shibutani M., Kajiwara T., Hase T.;
Submitted (Max-1996) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: Belongs to the cytochrome P450 family.
EMBL; U51674; AAA97465.1; -...
GO; GO:0016829; F:lyase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      479 AA; 54012 MW; ED6C06DAIDE81953 CRC64;
                                                               385 GYQPLVMKDPKVFDEPEKFVLERFTKEKGKELLNYLFW 422
                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            388 GYQPLVMKDPKVFDEPEKFVLERFTKEKGKELLNYLFW 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                               GTQPL-----ILAQFMRVGGDELLHFLLW 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTQPL------ILAQFMRVGGDELLHFLLW 25
  Score 50; DB 2;
Pred. No. 39;
5; Mismatches
                                                                                                                                   479 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 480 AA
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31.6%; Pred. No. 40;
tive 5; Mismatches
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                                                                                                                                                         01.NOV-1999 (TEMBLrel. 12, Crea
01.NOV-1999 (TEMBLEel. 12, Last
01-CCT-2003 (TEEMBLrel. 5, Last
Hydroperoxide lyase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fatty acid hydroperoxide lyase. Capsicum annuum (Bell pepper).
Query Match
Best Local Similarity 31.6%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 31.6
nes 12; Conservative
                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                         lamiids; Solanale
NCBI_TaxID=4081;
                                                                                                                                                                                                                                                                                                          TISSUE=Leaf
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Matches
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Q39443
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Q9XGI8
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Nicotiana attenuata.
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
NCBI_TaxID=49451;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Capsicum annuum (Bell pepper).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots, asterids;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-: SIMILARITY: Belongs to the cytochrome P450 family.
EMBL; AY028374 AAK27266.1; -.
PIR; S74228; S74228; Farbase activity; IEA.
GO; GO:0016829; F:Wase activity; IEA.
GO; GO:0016829; F:monoxygenase activity; IEA.
InterPro: IPR001128; Cytochrome_P450.
InterPro: IPR00128; Cytochrome_P450.
Ffam; PF00067; P450; 1.
PFAM; PF00065; EP4501V.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 37.9%; Score 50; DB 2; Length 480; Local Similarity 31.6%; Pred. No. 40; https://doi.org/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.10
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                                                                                                                                                                                                                                                                                                                                                       480 AA; 54056 MW; 84A2F646A55D46C9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     389 GYQPLVWKDPKVFDEPEKFMLERFTKEKGKELLNYLFW 426
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
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Pred. No. 40;
GO; GO:0004497; F:monooxygenase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR01128; Cytochrome_P450.
InterPro; IPR003403; EP450IV.
PRINTS; PR00465; EP450IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.9%; Scor.
31.6%; Pred. No. 40,
... 5; Mismatches
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NCBL_TaxID=4072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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Capsicum annuum (Bell pepper).
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MEDLINE=98344137; PubMed=9679194;
Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Kawarabayasi Y., Sawada M., Horikawa H., Takamiya M., Ohiuku Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohiuku Y.,
Punahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Makamura Y., Robb F.T., Horikoshi K.,
Masuchi Y., Shizuya H., Kikuchi H.,
Complete sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii OT3.",
DNA Res. 5:55-76(1998).
SEN: Aproxococus horikoshii OT3.",
DNA Res. 5:55-76(1998).
SEN: C71170, C71170.
GO; GO:001620; C:membrane; IEA.
GO; GO:001620; C:membrane; IEA.
RO; GO:00482; GSPII_F; Smottein secretion; IEA.
RICEPRO: IPRO01992; Bact_secr_systII.
Remi, PPO0482; GSPII_F; Smottein scretion;
Remiplere proteome; Hypothetical protein.
SEQUENCE 573 AA; 64304 WW; 91C98BGBEF45CC36 CRC64;
                                                                           Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
Parasitiformes; Ixodida; Ixodidae; Ixodes.
NCBL_TaxID=6945;
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SEQUENCE FROM N.A.
PAGNILA M., Guilfoile P.G.;
Packila M., Guilfoile P.G.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY224848; AA085921.1;
SEQUENCE 216 AA; 23990 MW; C9C97E9B331FE0AE CRC64;
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Last annotation update)
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Matches 10; Conservative
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NCBI_TaxID=53953;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
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Rhodopirellula baltica.
Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
Planctomycetaceae; Pirellula.
                                                                                                                              Siegler J.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
L. Submitted (SEP-2001) to the cytochrome P450 family.
R. GO; O:0016829; B:19ase activity; IEA.
R. GO; GO:0004497; F:monooxygenase activity; IEA.
R. GO; GO:000418; P:electron transport; IEA.
R. InterPro; IPR001128; Cytochrome_P450.
R. InterPro; IPR001403; E9450IV.
R. Pfam; PF00067; P450; 1.
R. PRINTS; PR00465; EP450IV.
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Complete proteome; Hypothetical protein.
SEQUENCE 188 AA; 21276 MW; 34C149E49889435C CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
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MEDLINE=22735913; PubMed=12835416;
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Best Local Similarity 31.6
Matches 12; Conservative
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                                        Keinaenen M.;
Submitted (OCT-2001)
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SEQUENCE FROM N.A.
STRAIN-BA71V;
MEDLINE-93281390; PubMed-8506138;
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MEDLINE=94243035; PubMed=8186465;
Gibbons B.H., Asai D.J., Tang W.J., Hays T.S., Gibbons I.R.;
"Phylogeny and expression of axonemal and cytoplasmic dynein genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and evolutionary relationships of African swine fever virus
                                                                                         Tripneusces gratilla (Hawaian sea urchin).
Eukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
Echinoidea, Euechinoidea, Echinacea, Temnopleuroida, Toxopneustidae,
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viruses, no RNA stage; Asfarviridae; Asfivirus.
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1078 AA; 121418 MW; 049AE4EA66316329 CRC64;
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50.0%; Pred. No. 1.3e+02;
tive 4; Mismatches 4; Indels
                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2004 (TrEMBLrel. 26, Last sannotation update)
Dynein heavy chain isotype 5A (EC 3.6.1.3) (Fragment).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                uncoupled; IEA.
  PRT; 1078 AA.
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GO; GO:0042624; F:ATP be activity, uncoupl
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:00166; F:hydrolase activity; IEA.
IMPREPE, IRRODS93; AAA_ATPase.
SMART; SM0382; AAA, ATPase.
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MEDLINE=90223993; PubMed=2327074;
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MEDLINE=90357780; PubMed=2389555;
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EMBL; U03977; AAAG5591.1; -.
PIR; T30879; T30879.
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Viruses; dsDNA viruses, no
NCBI_TaxID=10497;
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  PRELIMINARY;
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NCBI_TaxID=7673;
Q27807
Q27807;
01-NOV-1996 (
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Camacho A., Vinuela E.;
"Protein p22 of African swine fever virus: an early structural protein that is incorporated into the membrane of infected cells.";
Virology 181:251-257(1991).
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Virology 188:938-947(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=BA71V;
MEDLINE=20087485; PubMed=1309282;
MEDLINE=20087485; PubMed=1309282;
Gentiquez J.M., Salas M.L., Vinuela E.;
"Genes homologous to ubiquitin-conjugating proteins and eukaryotic transcription factor II in African swine fever virus.";
Virology 186:40-52(1992).
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Garcia-Beato R., Freije J.M.P., Lopez-Otin C., Blasco R., Vinuela
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MEDLINE=93346971; PubMed=8393914;
Manez R.J., Rodriguez J.M., Rodriguez J.F., Salas M.L., Vinuela E Yanez R.J., Abdriguez J.M., Rodriguez J.M., Rodriguez J. R., Salas M.L., Vinuela E Yanez R.J., Rodriguez J. Rodriguez J. Rodriguez J. Rodriguez J. Sequence and transcriptional mapping ", J. Gen. Virol. 74:1633-1638(1993).
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MEDLLINE=90219205; PubMed=2325203;
MEDLLINE=90219205; PubMed=2325203;
De La Vega I., Calvo V., Almazan F., Almendral J.M., Ramirez J.C.,
De La Vega I., Blasco R., Vinuela E.;
"Multigene families in African swine fever virus: Family 360.";
J. Virol. 64:2073-2081(1990).
                                       R., Vinuela E.;
ne fever virus: family 110.";
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MEDLINE=93174976; PubMed=8438592;
Marez R.J., Vinuela E.;
"African swine fever virus encodes a DNA ligase.";
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MEDLINE=93353606; PubWed=8102411;
Yane=Z R.J., Almazan F., Vinuela E., Rodriguez J.F.;
Yanez R.J., Almazan F., Vinuela E., Rodriguez J.F.;
African swine fever virus encodes a CD2 homolog responsible for the adhesion of eythrocytes to infected cells.";
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pl0 of African swine fever virus.";
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Rodriguez J.M., Yanez R.J., Rodriguez J.F., Vinuela E., Salas M.L.;
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sequence and transcriptional mapping.";
Gene 136:103-110(1993)
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Mapping and sequence of the gene encoding the African swine fever virion protein of Mr.) 11500.";
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MEDLINE=94085774; PubMed=8262374;
Yanez R.J., Rodriguez J.M., Boursnell M.E.G., Rodriguez J.F.,
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Pena L., Yanez R.J., Revilla Y., Vinuela E., Salas M.L.;
"African swine fever virus guanylyltransferase.";
Virology 193:319-328(1993).
                                                                                            Nucleic Acids Res. 21:2423-2427(1993).
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MEDLINE=93327788; PubMed=8335009;
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SEQUENCE FROM N.A.
MEDLINE=9904760; PubMed=9830033;
MEDLINE=9904760; PubMed=9830033;
Guenzi E., Galli G., Grgurina I., Gross D.C., Grandi G.;
"Characterization of the syringomycin synthetase gene cluster. A link between prokaryotic and eukaryotic peptide synthetases.";
between prokaryotic and eukaryotic peptide synthetases.";
-1. SimilaRITY: Belongs to the ATP-dependent AMP-binding enzyme
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RG GO: GO: 00048037; F: catalytic activity; IEA.

RG GO: GO: 0016788; F: hydrolase activity, acting on ester bonds; IEA.

RG GO: GO: 0016788; F: hydrolase activity, acting on ester bonds; IEA.

RG GO: GO: 00009058; P: hydrolase activity, acting on ester bonds; IEA.

R GO; GO: 00009058; P: hydrolase activity, acting on ester bonds; IEA.

R InterPro; IPR009081; ACP like.

R InterPro; IPR0091243; AMP-bind.

R InterPro; IPR0016124; Condensatn.

R InterPro; IPR001031; Thioesterase.

R Pfam; PF00501; AMP-binding; 8.

R Pfam; PF00501; AMP-binding; 8.
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MEDLINE=21820291; PubMed=11831707;
Yanez R.J., Rodriguez J.M., Nogal M.L., Yuste L., Enriquez C.,
Rodriguez J.F., Vinuela E.;
Analysis of the complete nucleotide sequence of African swine fever
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Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadaceae, Pseudomonas.
                                                                                             "Multigene families in African swine fever virus: family 505."; J. virol. 68:2746-2751(1994).
MEDLINE=94187118; PubMed=8139051;
Rodriguez J.M., Yanez R.J., Pan R., Rodriguez J.F., Salas M.L.,
Vinuela E.;
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Pred. No. 1.6e+02;
5; Mismatches 6; Indels
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAX-2004 (TrEMBLrel. 26, Last annotation update)
Syringomycin synthetase.
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HSSP; P14687; IAMU.
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DR Pfam; PF00550; PF-binding; 9.

DR Pfam; PF00975; Thicosterase; 1.

DR PRINTS; PR00154; Ambanding; 8.

DR TIGREAMS; TICR01733; AA-denyl-dom; 8.

DR PROSITE; PS000455; AMP_BINDING; 8.

DR PROSITE; PS00012; PHOSPHOPANTETHEINE; 5.

DR PROSITE; PS00012; PHOSPHOPANTETHEINE; 5.

KW Phosphopantetheine.

SQ SEQUENCE 9376 AA; 1029843 MW; P770C08975EP9CE5 CRC64;

Query Match

37.1%; Score 49; DB 2; Length 9376;

Best Local Similarity 43.5%; Pred. No. 1.3e+03;

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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## ALIGNMENT

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US-09-328-352-6394

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GENERAL THRORADION:

PAPELICLANT:

GARGEL TROPER CALD AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: UNCLETC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: DAYLEN CALD AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: DAYLEN CALD AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

CURRENT APPLICATION NUMBER: US09/328,352

CURRENT FILING DATE: 1999-06-04

INMURENE OF SEQ ID NOS: 8252

SEQ ID NOS: 8252

SEQ ID NOS: 8252

SEQ ID NOS: 8254

QUETY MATCH

BENTH: 534

QUETY MATCH

MATCHES IN THE SECONDATE CALD AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA:

INTERPRESENCE: 10719-7

GARGEL LACAL SAMINO: POR DIAGNOSTICS AND THERAPEUTICS

RESULT 2

RESULT 2

RESULT 2

RESULT 2

RESULT 2

RESULT 3

SEQ ID NOS: 82020

APPLICATION NUMBER: US09/248,796A

CURRENT FILING DATE: 1999-02-13

PRICE PETING DATE: 1999-02-13

NUMBER OF SEQ ID NOS: 82208

RECURRENT FILING DATE: 1999-02-13

NUMBER OF SEQ ID NOS: 82208

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Length 221;

DB 4;

Score 48.5;

30.7%;

TYPE: PRT ORGANISM: Candida albicans

US-09-248-796A-20200

Query Match

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Sequence 17390, Application US/09248796A

Patent No. 674137

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: 19709-02-12
CURRENT FAPLICATION NUMBER: US/09/248,796A
CURRENT FAPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 17390
LENGTH: 692
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Sequence 2848, Application US/09540236
Parent No. 6673910
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAFTILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION WUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
WUMBER OF SEQ ID NOS: 3840
SEQ ID NOS: 3840
SEQ ID NOS: 3840
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APPLICANT: GATY L. Breton et al.
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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Pred. No. 24;
6; Mismatches 9; Indels
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29.7%; Score 47; DB 4; Length 692;
Best Local Similarity 47.8%; Pred. No. 70;
Matches 11; Conservative 1; Mismatches 11; Indels
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171 NYKAAGDALGIDLLHNP 187
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Best Local Similarity 42.3%;
Matches 11; Conservative
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US-09-248-796A-17390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT; CACANISM: M.catarrhalis
US-09-540-236-2848
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                                                                                                            RESULT 5
US-09-540-236-2848
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ORGANISM: (
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US-09-252-991A-23329

US-09-252-991A-23329

Sequence 23329, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT NO. NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

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                                          Gaps
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| TITLE OF INVENTION: MITOMYCIN BY/09/266,965 CURRENT APPLICATION NUMBER: US/09/266,965 CURRENT FILING DATE: 1999-03-12 EARLIER APPLICATION NUMBER: PCT/US94/11279 EARLIER APPLICATION NUMBER: PCT/US94/11279 EARLIER APPLICATION NUMBER: US/08/133,963 EARLIER PILING DATE: 1993-10-07 NUMBER OF SEQ ID NOS: 145 SOTTWARE: FRUSEE FOR Windows Version 3.0 SOTTWARE: FRUSEE FOR Windows Version 3.0 SEQ ID NO 141 LENGTH: APPLICATION NUMBER OF SEQ ID NO 141 LENGTH: APPLICATION NUMBER OF SEQ ID NOS: 145 SEQ ID NO 141 LENGTH: APPLICATION NUMBER OF SEQ ID NO 141 LENGTH: APPLICATION NUMBER OF SEQ ID NOS: 145 SEQ ID NO 141 LENGTH: APPLICATION NUMBER OF SEQ ID NO 141 LENGTH: APPLICATION NUMBER OF SEQ ID NOS: 145 SEQ ID NO 141 LENGTH: APPLICATION NUMBER OF SEQ ID NOS: 145 SEQ ID NO 141 LENGTH: APPLICATION NUMBER OF SEQ ID NO 141 LENGTH: APPLICATION NUMBER OF SEQ ID NO 141 LENGTH: APPLICATION NUMBER OF SEQ ID NO 141 LENGTH: APPLICATION NUMBER OF SEQ ID NO 141 LENGTH: APPLICATION NUMBER OF SEQ ID NO 141 LENGTH: APPLICATION NUMBER OF SEQ ID NO 141 LENGTH: APPLICATION NUMBER OF SEQ ID NO 141 LENGTH: APPLICATION NUMBER OF SEQ ID NO 141 LENGTH: APPLICATION NUMBER OF SEQ ID NO 141 LENGTH: APPLICATION NUMBER OF SEQ ID NO 141 LENGTH: APPLICATION NUMBER OF SEQ ID NO 141 LENGTH: APPLICATION NUMBER OF SEQ ID NO 141 LENGTH: APPLICATION NUMBER OF SEQ ID NO 141 LENGTH: APPLICATION NUMBER OF SEQ ID NO 141 LENGTH: APPLICATION NUMBER OF SEQ ID NO 141 LENGTH: APPLICATION NUMBER OF SEQ ID NO 141 LENGTH: APPLICATION NUMBER OF SEQ ID NO 141 LENGTH: APPLICATION NUMBER OF SEQ ID NO 141 LENGTH: APPLICATION NUMBER OF SEQ ID NO 141 LENGTH: APPLICATION NUMBER OF SEQ ID NO 141 LENGTH: APPLICATION NUMBER OF SEQ ID NO 141 LENGTH: APPLICATION NUMBER OF SEQ ID NO 141 LENGTH: APPLICATION NUMBER OF SEQ ID NO 141 LENGTH:
                                          Indels
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30.4%; Score 48; DB
Best Local Similarity 40.6%; Pred. No. 26;
Matches 13; Conservative 7; Mismatches
   Best Local Similarity 37.5%; Pred. No. 9;
Matches 12; Conservative 5; Mismatches
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Patent No. 6495348
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23329
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Matches 9; Conserv
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Sequence 18090, Application US/09248796A
Sequence 18090, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/99/248,796A
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 18090
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Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;
FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62217

SOFTWARE: Patentin Ver. 2.0
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; Sequence 34186, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT; Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
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Pred. No. 1.1e+02;
4; Mismatches 8; Indels
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Best Local Similarity 41.7%; Pred. No. 16;
Matches 10; Conservative 5; Mismatches
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OTHER INFORMATION: Xaa means any amino acid US-09-270-767-34186
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ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 42.9%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18090
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US-09-270-767-49403
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US-09-270-767-34186
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LENGTH: 125
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Sequence 14297, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION: DECOME

APPLICANT: GATY Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CORRESSION OF THE REFERENCE: 2709-2004001

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR PRIOR DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

LENGTH: 63

LENGTH: 63
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### Pacent No. 6617156
### GENERAL INFORMATION:
### PAPLICATION:
UMBER: US/09/134,000C
### PRIOR PAPLICATION NUMBER: US/09/134,000C
### PRIOR PAPLICATION NUMBER: US/09/134,000C
### PRIOR PAPLICATION NUMBER: US/05,778
### PRIOR PAPLICATION NUMBER: US/05,778
### PRIOR PAPLICATION NUMBER: US/055,778
### PRIOR PAPLICATION NUMBER: US/05,778
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### PAPLICATION UMBER: US/055,778
### PAPLIC
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                                                                                                                                                                                           Score 46.5; DB 4; Length 523;
Pred. No. 58;
5; Mismatches 13; Indels 1:
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Pred. No. 58;
2; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 GFPGVTNFQVLL-AL-ASLIPTP 29
                                                                                             ) ORGANISM: Acinetobacter baumannii
US-09-328-352-6395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRGANISM: Enterococcus faecalis US-09-134-000C-3849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRGANISM: Klebsiella pneumoniae US-09-489-039A-14297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.1%;
56.5%;
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                                                                                                                                                                                           Query Match
Best Local Similarity 32.6%;
Matches 14; Conservative
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114 LNNFOKIADALTIS 127
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Best Local Similarity 64.3<sup>3</sup>
Matches 9; Conservative
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Matches 13; Conserv
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US-09-489-039A-14297
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SEQ ID NO 6395
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                                      LENGTH:
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225 GADPVTRFSLTRQVLNVGPRVPIGPNPVIT 254

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                                                                                                                                                                                                                           9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESCEE: Carella, Byrne, Bain, Gilfillan, ADRESSEE: Cacchi, Stewart & Olstein STREET: 6 Backer Farm Road CITY: Roseland STREET: 6 Backer Farm Road CITY: Roseland STATE: New Jersey COUNTY: USA ZIE: 07068
COMPUTER: 1BM PS/2
COMPUTER: 1BM PS/2
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COMPUTER: 1BM PS/2
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COMPUTER: 1BM PS/2
COMPUTER: 1BM PS/2
COMPUTER: 03/2010
SOFTWARE: 07-UN-1995
CLASSIFCATION NUMBER: 08/326,347
FILING DATE: 09-NOV-1992
APPLICATION NUMBER: 08/973,307
FILING DATE: 09-NOV-1992
APTORNEY AGENT INCORMATION:
NUMBER: 13/4 APPLICATION NUMBER: 08/973,307
FILING DATE: 09-NOV-1992
ATTORNEY AGENT INCORMATION:
NUMBER: 13/4 APPLICATION NUMBER: 08/973,307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Anderson, W. French
APPLICANT: Baltrucki, Leon F.
APPLICANT: Mason, James M.
TITLE OF INVENTION: Targetable Vector Particles
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 45; DB 2
Pred. No. 84;
5; Mismatches
                                                                                                                                                                          Query Match 28.5%; Score 45; DB Best Local Similarity 41.7%; Pred. No. 16; Matches 10; Conservative 5; Mismatches
                                                                                                           ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-49403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           271010-281
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                                                                                                                                                                                                                                                                                             26 NTVNARNLINHFSVVRIPLNIKLM 49
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08484126
Patent No. 5985655
GENERAL INFORMATION:
                                                                 ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 453 amino acids
TYPE: amino acid
STRANDEDNESS:
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Best Local Similarity 33.3
Matches 10; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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SEQ ID NO 49403
LENGTH: 125
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US-08-484-126-3
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                                            TYPE: PRT
                                                                                        FEATURE:
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Sequence 15218, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL OF INVENTION:
TITLE OF INVENTION:
FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE:
CURRENT APPLICATION NUMBER:
US/09/248,796A
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            Sequence 3, Application US/09374909

Patent No. 6603501

GENERAL INFORMATION:
GENERAL INFORMATION:
MASON, James M.

TITLE OF INVENTION: Targetable Vector Particles
NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
ADDRESSE: Carella, Stewart & Olstein
STREET: 6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/374,909
FILING DATE: 13-Aug-1999
CLASSIFICATION: cluknown>
PRIOR APPLICATION NUMBER: 08/484,126
FILING DATE: cluknown>
APPLICATION NUMBER: 08/973,307
FILING DATE: cluknown>
APPLICATION NUMBER: 08/973,307
FILING DATE: 09-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Lillie, Raymond J.
REGISTRATION NUMBER: 31,778
TELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225 GADPVTRFSLTRQVLNVGPRVPIGPNPVIT 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: xenotropic gp70 protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 GFDLITNFQVVADALNIS----LLPNPLAT 31
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 453 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                  CITY: Roseland
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 10; Conserval
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US-09-248-796A-15218
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JS-09-374-909-3
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Gaps

11; Indels

6 GFDLITNFOVVADALNIS----LLPNPLAT 31

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131609,

Sequence Sequence Sequence

Sequence 183864, Sequence 139, App Sequence 141, App Sequence 141, App Sequence 141, App Sequence 131113, Sequence 13153, Sequence 13153, Sequence 13153, Sequence 13153, Sequence 13122, Sequence 15293, Sequence 15293, Sequence 241734, Sequence 25334, Sequence 25336, Sequence 25417, A Sequence 25417, A Sequence 25417, A Sequence 25417, A Sequence 25417, A Sequence 25417, A Sequence 25417, A Sequence 25417, A Sequence 25417, A Sequence 25417, A Sequence 25417, A Sequence 25417, App Sequence 4754, App Sequence 475,  
Seguence 129864,

ALIGNMENTS

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Fri Nov 12 14:55:55 2004
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Title:

Run

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Sequence (5), Application US/10092750;
Sequence (5), Application No. US200300321574];
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hammond, Philip W.
APPLICANT: Alpin, Julia
TITLE OF INVENTION: POLYPEPTIGES INteractive with BCL-XI
FILE REFERENCE: 50036/050002
CURRENT FILE OF INVENTION: DOLYPEPTIGES:
CURRENT APPLICATION NUMBER: US/10/092,750
CURRENT FILING DATE: 2002-03-07
PRIOR FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 253
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 67
LENGTH: 32
US-10-425-115-355295

US-10-437-963-112368

US-10-437-963-112368

US-10-424-599-1838649

US-10-425-066A-456

US-10-225-066A-456

US-10-225-066A-456

US-10-225-066A-456

US-10-225-066A-456

US-10-225-066A-456

US-10-225-11313

US-10-369-493-113638

US-10-437-963-1131315

US-10-425-115-24468

US-10-425-115-24468

US-10-425-115-264831

US-10-425-115-264831

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US-10-425-115-264831

US-10-425-115-264831
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US-10-334-143-42
US-10-437-963-119426
US-10-437-963-129864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MDTIKGFDLITNFOVVADALNISLLPNFLATA 32
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      US-10-424-599-156639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -10-092-750-67
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Sequence 156639,
Sequence 186736,
Sequence 182955,
Sequence 243733,
Sequence 45323,
Sequence 45323,
Sequence 45323,
Sequence 189437,
Sequence 252020,
Sequence 24320,
Sequence 24320,
Sequence 24320,
                                                                                                                                                                                                                                              (without alignments)
146.426 Million cell updates/sec
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                                                                                                                                                                                                                 November 11, 2004, 02:43:24 ; Search time 77.3238 Seconds
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1: /cgn2_6/ptodatca/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodatca/2/pubpaa/PCT_RW PUBL.pep:*
4: /cgn2_6/ptodatca/2/pubpaa/US06_NBW PUB.pep:*
4: /cgn2_6/ptodatca/2/pubpaa/US06_NBW PUB.pep:*
5: /cgn2_6/ptodatca/2/pubpaa/US06_NBW PUB.pep:*
6: /cgn2_6/ptodatca/2/pubpaa/US08_NBW PUB.pep:*
7: /cgn2_6/ptodatca/2/pubpaa/US08_NBW PUB.pep:*
8: /cgn2_6/ptodatca/2/pubpaa/US08_NBW PUB.pep:*
9: /cgn2_6/ptodatca/2/pubpaa/US08_PUBCOMB.pep:*
10: /cgn2_6/ptodatca/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodatca/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodatca/2/pubpaa/US09_NBW PUB.pep:*
12: /cgn2_6/ptodatca/2/pubpaa/US09_NBW PUB.pep:*
13: /cgn2_6/ptodatca/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodatca/2/pubpaa/US10A_PUBCOMB.pep:*
15: /cgn2_6/ptodatca/2/pubpaa/US10P_PUBCOMB.pep:*
16: /cgn2_6/ptodatca/2/pubpaa/US10P_PUBCOMB.pep:*
17: /cgn2_6/ptodatca/2/pubpaa/US10P_PUBCOMB.pep:*
18: /cgn2_6/ptodatca/2/pubpaa/US10_PUBCOMB.pep:*
19: /cgn2_6/ptodatca/2/pubpaa/US10_PUBCOMB.pep:*
                                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-092-750-67
US-10-424-599-156639
US-10-425-115-36776
US-10-425-115-285776
US-10-425-115-243733
US-10-425-115-243733
US-10-425-115-243733
US-10-425-115-316100
US-10-767-701-42726
US-10-767-701-42726
US-10-767-305-115-262020
US-10-267-305-133
                                                                                                                                                                                                                                                                                                                                                                  158
1 MDTIKGFDLITNFQVVADALNISLLPNPLATA 32
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Gaps

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Indels

Length 32;

Result

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APPLICANT: La Rosa, Thomas J.
APPLICANT: Exercise David K.
APPLICANT: Shou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Wei
APPLICANT: Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 122995
LENGTH: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: LA ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yahua
APPLICANT: Cao, Vongwei
TITLE OF INVENTION: Wolclet Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION WUMBER: US/10/425,115
CURRENT FILING DATE: 2003-64-28
NUMBER OF SEQ ID NOS: 369326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Indels
                                                                                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: Clone ID: PAT_MRT3847_142295C.1.pep
US-10-424-599-189678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: PAT_MRT4530_25872C.1.pep
US-10-437-963-122995
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
32.3%; Score 51; DB 15;
Best Local Similarity 46.2%; Pred. No. 1.5e+02;
Matches 12; Conservative 3; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 50; DB 16;
Pred. No. 14;
                                                                                                                                                                                                                                                   LOCATION: (1)..(1097)
OTHER INFORMATION: unsure at all Xaa locations
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Publication No. US20040214272A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 122995, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
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32 RVVADAALLSLSPSPLA 48
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Best Local Similarity 64.7%;
Matches 11; Conservative
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 189678
LENGTH: 1097
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                                                                                                          TYPE: PRT ORGANISM: Glycine max FEATURE: NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-437-963-122995
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US-10-425-115-243733
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
ESEQ ID NO 156639
LENGTH: 254
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US-10-424-599-188678
US-10-424-599-188678
Sequence 189678, Application US/10424599
Sublication No. US20040031072A1
GENBRAL INFORMATION:
GENBRAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFRENCE: 38-21 (53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 367776, Application US/10425115
Publication No. US20040214272A1
Fublication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yondae
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APPLICANT: Cao, Yondae
APPLICANT: Cao, Yondae
APPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: PAT_MRT3847_112466C.1.pep
US-10-424-599-156639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: MRT4577_98584C.1.pep
US-10-425-115-367776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 TIKGFDLITNFQVVADALNISLLPNPL 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -10-425-115-367776
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Sequence 189437, Application US/10437963
; Sequence 189437, Application US/10437963
; Publication No. US20040123343A1
; Bublication No. US20040123343A1
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Cao, Yongwei
; APPLICANT: Cao, Yongwei
; APPLICANT: Barbazuk, Brad
; APPLICANT: Barbazuk, Brad
; APPLICANT: Barbazuk, Brad
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5321) B
; CURRENT APPLICATION NUMBER: US/10/437,963
; UNMBER OF SEQ ID NOS: 204966
; SEQ ID NO 189437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 42726, Application US/10767701
Publication No. US20040172684A1
Publication No. US20040172684A1
Publication No. US20040172684A1
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21 (53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT APPLICATION SEQ ID NOS: 63128
SEQ ID NO 42726
                                                                                                 Gaps
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                       ch 31.0%; Score 49; DB 17; Length 87; 1 Similarity 54.5%; Pred. No. 13; 12; Conservative 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 49; DB 16; Length 55: Pred. No. 1.38+02; 7; Indels
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US-10-767-701-42726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: PAT_MRT4530_85948C.1.pep
US-10-437-963-189437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
31.0%; Score 49; DB
Best Local Similarity 42.9%; Pred. No. 1.3e
Matches 9; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
30.7%; Score 48.5; D
Best Local Similarity 40.0%; Pred. No. 45;
Matches 12; Conservative 3; Mismatches
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                                                                                                                                                         11 TNFQVVADALNISLLPNPLATA 32
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ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Oryza sativa
                                 Query Match
Best Local S:
Matches 12,
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; Sequence 316100, Application US/10425115
; Publication Wo. US2004021427241
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: La Royalc, David K.
; APPLICANT: Zhou, Yihna
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; TITLE REFERENCE: 38-21 (53222)
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 316100
; LENGTH: 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 45323, Application US/10425114

| Sequence 45323, Application US/10425114
| Publication No. US20040034888A1
| Publication No. US20040034888A1
| GENERAL INFORMATION:
| APPLICANT: Zhou, Yihua |
| APPLICANT: Screen, Steven E |
| APPLICANT: Tabaska, Jack E |
| APPLICANT: Tabaska, Jack E |
| APPLICANT: Tabaska, Jack E |
| APPLICANT: Tabaska, Jack E |
| APPLICANT: Tabaska, Jack E |
| APPLICANT: Tabaska, Jack E |
| APPLICANT: Tabaska, Jack E |
| APPLICANT: Cao, Yongwei |
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With |
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With |
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With |
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With |
| TITLE OF INVENTION: NUMBER: US/10/425,114 |
| CURRENT FILING DATE: 2003-04-28 |
| SEQ ID NOS: 73128 |
| SEQ ID NO 45323 |
| ENGARCH ACID NO 45
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                                                                                                                                                                                                                                                 DB 17; Length 426;
64;
                                                                                                                                                                                                                                                                                                                6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: UC-ZMFLMO17201A01_FLI.pep
US-10-425-114-45323
                                                                                                                     ; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_153867C.1.pep
US-10-425-115-243733
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                                                                                                                                                                                                                                                 Score 50; DB 1; Pred. No. 64; 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31.6%; Score 50; DB ilarity 43.5%; Pred. No. 66; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     304 ELVAGOKIVSEALKISLLSDPRA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  313 ELVAGOKIVSEALKISLLSDPRA 335
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                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 43.5%;
Matches 10; Conservative
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Best Local Similarity
Matches 10; Conserv?
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ORGANISM: Zea mays
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ORGANISM: Zea mays
                                                            TYPE: PRT
ORGANISM: Zea mays
SEQ ID NO 243733
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-267-502-242
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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                                                                                                               Squares 202020, Application US/10425115
; Squares 202020, Application US/10425115
; Publication No. US20040214272A1
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Royalic, David K.
; APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Can Yongwai
; APPLICANT: Application Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Number: US/10/425,115
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 262020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 35.5%; Pred. No. 59;
Matches 11; Conservative 7; Mismatches 10; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 133, Application US/10263929;
Publication No. US20040067535A1
GENERAL INFORMATION:
APPLICANT: Galant, Ron
TITLE OF INVENTION: Albheimer's Disease Linked Genes
FILE REFERENCE: LSD-07417
CURRENT APPLICATION NUMBER: US/10/263,929
CURRENT FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 213
SOFTWARE: Patentin version 3.2
SEQ ID NO 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , OTHER INFORMATION: Clone ID: MRT4577_170575C.1.pep
US-10-425-115-262020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: unsure
LOCATION: (1)..(260)
OTHER INFORMATION: unsure at all Xaa locations
PEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |:||||||
TVKGFDL-----NLVPAPAATA 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-263-929-133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Zea mays
                                                                                           RESULT 11
US-10-425-115-262020
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US-10-267-502-242 ; Sequence 242, Application US/10267502 ; Publication No. US20040071700A1 ; GENERAL INFORMATION:

RESULT 13

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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53221) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-425-115-355295
; Sequence 355295. Application US/10425115
; Sequence 355295. Application US/10425115
; Publication No. US2004021427241
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; TITLE REFERENCE: 38-21 (52322) B
; CURRENT APLICATION NUMBER: US/10/425,115
; CURRENT APLICATION NUMBER: US/10/425,115
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 355295
; LENGTH: 56
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                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                           Query Match 30.7%; Score 48.5; DB 15; Best Local Similarity 34.5%; Pred. No. 6.5e+02; Matches 10; Conservative 7; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ), OTHER INFORMATION: Clone ID: MRT4577_87197C.1.pep
US-10-425-115-355295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 48; DB
Pred. No. 11;
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APPLICANT: Kim, Jaeseob
APPLICANT: Galant, Ron
TILE OF INVENTION: Obesity Linked Genes
FILE REFERENCE: LSD-07416
CURRENT APPLICATION NUMBER: US/10/267,502
CURRENT FILING DATE: 2003-01-27
NUMBER OF SEQ ID NOS: 439
SOFTWARE: Patentin version 3.2
LENGTH: 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                              2 DTIKGFDLITNFQVVADALNISLLPNPLA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-10-437-963-172368
is Sequence 172368, Application US/10437963
publication No. US20040123343A1
is GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
is APPLICANT: Pind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 NFQVVADALNISLLPNP 28
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Best Local Similarity 52.97
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; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 12368
; LENGTH: 231
; TENGTH: 231
; FEATURE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_70510C.1.pep
US-10-437-963-172368
Query Match
Best Local Similarity 48.3%; Pred. No. 61;
Matches 14; Conservative 2; Mismatches 11; Indels 2; Gaps 1;

Qy
6 GFDLITNFQVVADALNISLLEN--PLATA 32
Db
15 GFDLTANFQVVADALNISLLEN--PLATA 32
Db
15 GFDLTANFQVADALNISLLEN--PLATA 32
Db
15 GFDLTANFQVADALNISLLEN--THATA 32
Db
16 GFDLTANFQVADALNISLLEN--THATA 32
Db
17.3238 secs
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This Page Blom, luspio

us-10-092-750-67.rpr

OM protein - protein search, using sw model

November 10, 2004, 14:52:32; Search time 10.9324 Seconds (without alignments) 281.634 Million cell updates/sec Run on:

US-10-092-750-67 158 1 MDTIKGFDLITNFQVVADALNISLLPNPLATA 32 Perfect score: Title:

Sequence:

BLOSUM62

Scoring table:

283416 seqs, 96216763 residues Gapop 10.0 , Gapext 0.5 Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		a			SOUTHWITES	
Result		Query				
No.	Score	Match	Length	DB.	QI	Description
	52	32.9	(2)	7	0	oth
2	٥.	ď	9	7	m	hypothetical prote
m	50.5	3	624	7	T28423	ORF MSV261 leucine
4	49	31.0	481	~	A33712	metalloproteinase
Ŋ	œ	0	S	н	S04899	myb-related protei
9	48.5	0	360	7	A49700	ldehyde-
7	œ	30.7	Φ	Ŋ	AH1220	se h
œ		ö	418	0	802138	arginine deiminase
თ		30.4	636	Н	VCVWFS	env polyprotein -
10		30.4	931	N	S13580	collagen alpha 1(I
11	48	30.4	1411	(1)	S55123	hypothetical prote
12	7	ö	618	N	AC1204	phosphotransferase
13	47.5	30.1	791	N	D90988	hypothetical prote
14	7.	0	935	~	F85833	
15		30.1	1105	7	B64973	yegE protein - Esc
16	47	φ.	174	7	AH1979	_
	47	σı,	236	7	T48518	•
		٥.	240	N	B64063	nasD protein homol
	47	6.	243	~	T32906	hypothetical prote
		φ.	296	~	T35345	ഗ
	47	9	478	0	JN0892	metalloproteinase
	47	φ.	714	N	AH2366	hypothetical prote
	47	ď.	753	~	D81219	ğ
	47	6.	756	N	AB1088	chitinase B homolo
	47	6	756	~	AB1452	chitinase B homolo
	47	٩.	920	0	B34493	collagen alpha 1(I
	47	σ.	921	7	S40495	collagen alpha 1(I
28	47	ο.	921	7	842617	collagen alpha 1(I
	46.5	29.4	644	7	154	gp70 protein - mur

ري د

Gaps

3;

Query Match

32.0%; Score 50.5; DB 2; Length 268;
Best Local Similarity 40.6%; Pred. No. 9.2;
Matches 13; Conservative 8; Mismatches 8; Indels

capsule synthesis flagellar basal-bo flagellar basal-bo	env polyprotein, r undecaprenyl-phosp env polyprotein	Conserved nypotnet hypothetical prote probable cytochrom env polyprotein -	env polyprotenn - hypothetical prote periplasmic-bindin	rod shape-determin retrovirus-related probable integral
B47615 AC2644 C97426	B29350 G97253 VCMVSR	G90431 T31203 T07113 VCVWM2	VCVWM1 T22759 AH0297	D69502 S26840 E81450
0 0 0	00 H	2001	100	000
7 60 7 60 7 60 7 60	312 344 408	4 4 4 6 2 0 0 0 3 0 0 0	640 2824 323	363 1009 352
29.1 29.1 29.1	29.1	29.1 29.1 1.1.0 1.1.0 1.1.0	29.1	28.8 28.8 28.2
4 4 4 6 6 6	4 4 4 6 6 6	9 4 4 4 9 6 6 6	46 45.5	45.5 45.5 45
30 31 35	6 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8		4 4 4 0 4 2	4 4 4 6 4 0

## ALIGNMENTS

	RESULT 1
	hypothetical protein APE1034 - Aeropyrum pernix (strain K1)
	C)Species: Actorylum peints C)Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
	C.)ACCESION: V.7./V. V.7. Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Taka R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, T.; Kudoh, Y.; Yamazaki, J.; awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
	DNA Res. 6, 83-101, 1999 A. Title: Complete ganome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy A. Title: Complete ganome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy A. Defenence number. 272460. MITD: 043101349. DMID: 10382666
	A;Accession: (72702 A;Status: preliminary
	A;Molecule type: DNA A:Regidueg: 1-321 <kaw></kaw>
	A;Cross-references: UNIPROT:Q9YD78; DDBJ:AP000060; NID:g5104188; PIDN:BAA80019.1; PID:g
	C, Ganetican Control C
	Ajdene: Arkius4 CjSuperfamily: Aeropyrum pernix hypothetical protein APE1034
	Query Match Best Local Similarity 34.5%; Pred. No. 6.8; Matches 10; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
	Qy 4 IKGFDLITNFQVVADALNISLLPNPLATA 32
	Db 270 VEGFDVVPVDEPVVECLQLRLIGHPVARA 298
	RESULT 2 T12739
	hypothetical protein 23 - Methanobacterium phage psiM2 C;Species: Methanobacterium phage psiM2
	C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_cnange 09-Jui-zou4 C;Accession: T12739
	R;Pfister, P.; Wasserfallen, A.; Stettler, R.; Leisinger, T. submitted to the EMBL Data Library, May 1998
	A;Description: Archaeophage PsiM2 complete genomic DNA. A;Reference number: Z17578
	A;Accession: T12739 S;Status: translated from GB/EMBL/DDBJ S;Anjerile tyme: NN
	A; Residues: 1768 < PFI. A; Cross-references: UNIPROT:080213; EMBL:AF065411; NID:g3249585; PID:g3249608; PIDN:AAC A; Cross-references: Nost Methanobacterium thermoautotrophicum strain Marburg C; Superfamily: Methanobacterium phage psiM2 hypothetical protein 23
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myb-related protein Zm38 - maize

(Species: Zea mays (maize)

(Species: Zea mays (maize)

(Jate: 22e-1990 #sequence_revision 28-Peb-1990 #text_change 09-Jul-2004

(Jacession: 804899

R,Marocco, A.; Wissenbach, M.; Becker, D.; Paz-Ares, J.; Saedler, H.; Salamini, F.; Rohc

Mol. Gen. Genet. 216, 183-187, 1989

A,Title: Multiple genes are transcribed in Hordeum vulgare and Zea mays that carry the R,Reference number: 804899

A,Accession: 804899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Markos, A.; Miretsky, A.; Mueller, M.
J. Mol. Evol. 37, 631-643, 1993
A;Title. A glycaraldehyde-3-phosphate dehydrogenase with eubacterial features in the sA;Teference number: A49700; MUID:94157936; PMID:8114116
A;Accession: A49700
A;Molecule type: mRNA
A;Residues: 1-360 <AMAX
A;Cross-references: UNIPROT:Q27820; GB:L11394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: not compared with conceptual translation
A;Status: not compared with conceptual translation
A;Status: 1-255 < MAR>
A;Residues: 1-255 < MAR>
A;Cross-references: UNIPROT:P20025
C;Superfamily: barley myb-related protein 1; myb DNA-binding repeat homology
C;Reywords: DNA binding; duplication; nucleus; transcription regulation
E;9-61,Domain: myb DNA-binding repeat homology < MYB1>
F;6-112/Domain: myb DNA-binding repeat homology < MYB2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.Species: Trichomonas vaginalis
C.Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C.Accession: A49700; B44516; A44516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oxidoreductase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   compared with conceptual translation
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C;Kwywodes: gluconeogenseis; glycolysis; homotetramer; NAD;
F;3-35/Region: beta-alpha-beta NAD nucleoride-binding fold
F;171,198/Active site: Cys, His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Accession: B44516
A,Status: preliminary; not compared with conceptual transl
A,Molecule type: mRNA
A,Residues: 11-360 <MUW>
A,Crossdues: 160 <MUW>
A,Crossdues: 180 <MUM>
MUM
B,Muller, M.
Submitted to the Protein Sequence Database, February 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :| | :| : | | | | 1
119 RGIDPVTHRPIAADAVTVTTVSFQPSPSAAA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 KGFDLITNFQVVADAL---NISLLPNPLATA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 48.5; D
Pred. No. 17;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
30.7%; Score 48.5; E
Best Local Similarity 39.3%; Pred. No. 26;
Matches 11; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      299 DPIVSSDIIGCQYSSIVDALSTKVLPNP 326
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399 TVSAYDWITDFQTGIDKIDLSAFRN 423
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A;Molecule type: protein
A;Residues: 1-19,'X',21-63 <MUL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 35.5
Matches 11; Conservative
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Nylternate names: neutral protesse large subunit
(%)Alternate names: neutral protesse large subunit
(%)Alternate names: neutral protesse large subunit
(%)Accession: A3312, T48669
(%)Accession: A3312, T48669
(%) Piologopalaire, P.; Wandersman, C.
(%) Biol. Chem. 264, 9083-9089, 1089
(%) Arcession: A3312, MUID:89255387; PMID:2722818
(%) Arcession: A3312, MUID:89255387; PMID:2722818
(%) Arcession: A3312, MUID:89255387; PMID:2722818
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(%) Arcession: A3312, Mulderan, C.
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                                                                                                                                                                                                                                                                                                                                                          C;Species: Melanoplus sarguinipes entomopoxylus

C;Date: 21-dan-2000 #sequence_revision 21-dan-2000 #text_change 09-dul-2004

C;Accession: T28423

A;Title: The genome of Melanoplus sanguinipes entomopoxylus.

A;Reference number: 220484; MulD:99102612; PMID:9847359

A;Accession: T28423

A;Accession: T284423

A;Accession: T28423

A;Accession: T28423

A;Accession: T284423

A;Accession: T28423

A;Accession: T
                                                                                                                                                                                                                                                                                                                             ORF MSV261 leucine rich repeat gene family protein - Melanoplus sanguinipes entomopoxvid
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                                                                                                                                                                                                                                                                                                                                                Species: Melanoplus sanguinipes entomopoxvirus
Species: Al-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
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                                                           29 DTIKGYALLKNTGDEVIEDLL-IMPVPDFFAS 59
    DTIKGFDLITNF--QVVADALNISLLPNPLAT 31
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Pred. No. 31;
6; Mismatches
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Pred. No. 25;
4; Mismatches
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Best Local Similarity 36.0%;
Matches 9; Conservative
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Best Local Similarity 38.7%;
Matches 12; Conservative
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S13580 collagen alpha 1(IX) chain precursor, long splice form - human
NyAlernate names: procollagen alpha 1(IX) chain, long splice form
C;Species: Homo saplens (man)
C;Species: Homo saplens (man)
C;Species: Homo saplens (man)
C;Date: 13-1995 #sequence revision 10-Feb-1995 #text change 09-Jul-2004
C;Accession: $13580; $23295; $202140; $23580; $21087; $74\bar{7}94
R;Muragaki, Y.; Kimura, T.; Ninomiya, Y.; Olsen, B.R.
Bur. J. Biochem. 193.
R;Muragaki, Y.; Kimura, T.; Ninomiya, Y.; Olsen, B.R.
R;Ninomiser: $13580; MUD: 91006164; PMID: 2209617
A;Recession: $13580
A;Molecule type: mRNA
A;Residues: 1-331 «MURA
A;Recession: $13580; MUPROT: P20849; EMBL: X54412; NID: 930083; PIDN: CAA38276.1; PID: 93008
A;Ninomiya, Y.; Castagnola, P.; Gerecke, D.; Gordon, M.K.; Jacenko, O.; LuValle, P.; Mc
maguchi, N.; Olsen, B.R.
A;Title: The molecular matrix Genes, Sandell L.J. and Boyd C.D., eds., pp.79-114, Academic Pr
A;Title: The molecular biology of collagens with short triple-helical domains.
A;Recession: $23295
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-253, YV, 255-815;835-884 «NIN>
A;Residues: 1-253, YV, 255-815;835-884 «NIN>
Bur. J Biochem. 179, 71-78, 1989
A;Title: Molecular cloning of rat and human type IX collagen cDNA and localization of the A;Title: Molecular cloning of rat and human type IX collagen cDNA and localization of the A; Residues: $00140; MUD: 89137096; PMID: 2465149
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A;Accession: S02140
A;Accession: S02140
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 580-596,598-620, "R', 622-813;835-884 «KIM»
A;Residues: 580-596,598-620, "R', 622-813;835-884 «KIM»
B;Muragaki, Y:, Nishimura, I:, Henney, A.; Ninomiya, Y.; Olsen, B.R.
Proc. Natl. Acad. Sci. U.S.A. 87, 2400-2464, 1990
A;Title: The alphal(IX) collagen gene gives rise to two different tr.
A;Reference number: A35980; MUID:90207204; PMID:1690886
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crightine deiminase (EC 3.5.3.6) - Pseudomonas aeruginosa
C.Date: 01-Dec.1989 #sequence_revision 01-Dec.1989 #text_change 09-Jul-2004
C.Aaccession: S02138; B82999
R.Bur. H.; Luechi, E.; Stalon, V.; Mercenier, A.; Haas, D.
Bur. J. Bicchem. 179, 53-60, 1389
A.Title: Sequence analysis and expression of the arginine-deiminase and carbamate-kinase
A.Accession: S02137; MUD:89137094; PMID:2537202
A.Accession: S02137; MUD:89137094; PMID:2537202
A.Accession: S02137; MUD:89137094; PMID:2537202
A.Accession: S02138
A.Note: Date Change Control of the mature procein, was confit
A.Note: part of this sequence, including the amino end of the mature procein, was confit
A.Note: part of this sequence, including the amino end of the mature procein, was confit
A.Note: part of this sequence, including the amino end of the mature procein, was confit
A.Note: part of this sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A.Note: preliminary
A.Note: preliminary
A.Molecule type: DNA
A.Residues: 1-418 <500
A.Accession: B82993
A.Scatus Preliminary
A.Molecule type: DNA
A.Residues: 1-418 <500
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Accestate kinase homolog AckA2 [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Stecession: A4120
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J. Dominguez-Bernal, G.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.
D; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, P.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mackenter comparative genomics of Listeria species.
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUD:21537279; PMID:11679669
A;Status: preliminary
A;Molecule type: DNA
A;Residues: L-397 cdLa>
A;Cross-references: UniPROT: QBY7V1; GB:NC_003210; PIDN:CAC99246.1; PID:g16410584; GSPDB: A;Cross-references: UniPROT: Catalonate kinase
C;Genetics:
A;Genetics:
A;Genet
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C;Superfamily: arginine deiminase arcA
C;Keywords: hydrolase
F;2-418/Product: arginine deiminase #status predicted <WAT>
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7; Mismatches
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ilarity 28.9%;
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C,Accession: AC1204
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J. Doninquez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitcurnam, A.; McA, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-618 <GLA>
A;Cross-references: UNIPROT;Q8Y882; GB:NC_003210; PIDN:CAC99113.1; PID:g16410437; GSPDB
A;Experimental source: strain EGD-e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   partial probable sensor kinase 23236 [imported] - Escherichia coli (strain 0157:H7, sub
C,Species: Escherichia coli
C,Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Aug-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nypothetical protein ECs2876 [imported] - Escherichia coli (strain O157:H7, substrain R
                                                                                                                                                                                                                      phosphotransferase system (PTS) beta-glucoside-specific enzyme IIABC homolog lmo1035
                                                                                                                                                                                                                                                           C,Species: Listeria monocytogenes
C,Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.Species: Escherichia coli
C.Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 16-Aug-2004
C.Accession: D90988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Genetics:
A;Gene: lmo1035
C;Superfamily: phosphotransferase system enzyme II sucrose-specific;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: BCs2876
C;Superfamily: Signal transduction protein with an integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 791;
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                                     1294 VDNIEGVTFELDDLKRILVESLKLSLIPDP 1323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MDTIK--GFD-----LITNFQVVADALNISL 24
28
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Best Local Similarity 48.3%; Pred. No. 92;
Matches 14; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 47.5;
Pred. No. 69;
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1 MDTIKG--FDLITNFOVVADALNISLLPNP
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Best Local Similarity 35.5
Matches 11; Conservative
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A;Molecule type: DNA
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hypothetical protein YMR176w - yeast (Saccharomyces cerevisiae)

hypothetical protein YMR176w - yeast (Saccharomyces cerevisiae)

c) Species: Saccharomyces cerevisiae

C; Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004

C; Accession: S55123

R; Churcher, C.M.

submitted to the EMBL Data Library, June 1995

A; Recreace number: S5518

A; Accession: S5513

A; Molecule type: DNA

A; Recreace number: S5518

A; Molecule type: DNA

A; Recreaces: UNIPROT: Q03214; EMBL: Z49808; NID: 9854440; PIDN: CAA89909.1; PID: 98544

A; Experimental source: strain AB972

C; Genetics:

A; Gene: SGD: ECMS

A; Cross-references: SGD: S0004788; MIPS: YMR176w

A; Map position: 13R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Map position: 6412-6614

A Introns: 5/2; 232/3; 260/3; 267/3

C Complex: type IX collagen may be a heterotrimer of one alpha 1(IX) chain, one alpha 2(C Punction:

A; Description: structural component of extracellular fibrous polymer associated with typhotoe: in chondrocytes the long splice form is predominantly produced cikepwords: alternative splicing; coiled coil; extracellular matrix; glycoprotein, heter c; 47-49-31/Product: collagen alpha 1(IX) chain, long splice form #status predicted coiled coils f; 24-268/Domain: non-collagenous NC4 #status predicted coils

F; 269-405/Domain: non-collagenous COil #status predicted coils

F; 757-766/Domain: collagenous COIL #status predicted coils

F; 757-766/Domain: collagenous NC2 #status predicted coils

F; 757-766/Domain: collagenous NC2 #status predicted coils

F; 757-766/Domain: collagenous NC1 #status predicted coils

F; 771/Domain: collagenous NC1 #status predicted coils

F; 771/Domain: collagenous NC1 #status predicted coils

F; 771/Domain: non-collagenous NC1 #status predicted coils

F; 771/Didining site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                A)Reference number: S21087
A)Reference number: S21087
A)Rolecule type: DNA
A)Reference number: S21087
A)Rolecule type: DNA
A)Residues: 1-4;233-284, 7',250-267 < CLS>
A)Rolecule type: DNA
A)Residues: 1-4;233-284, 7',250-267 < CLS>
A)Rolecule type: DNA
A)Reference number: BMBL:M32135
B)Rochem J: 314, 327-332, 1996
B)RyTitle: Collagen type: IX from human cartilage: a structural profile of intermolecular of the Reference number: S44673; MUID:96195147; PMID:8660302
A)Reference number: Brockein
A)Rolecule type: procein
A)Rolecule type: procein
A)Rolecule type: Drocein
A)Rolecule type: Drocein
A)Rolecule type: All collagen the third position of the tripeptide repeating unit ed and subsequently O-glycosylated.
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64.3%; Pred. No. 94;
iive 2; Mismatches 3; Indels
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Best Local Similarity 33.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 11; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Gene: GDB:COL9A1
A,Cross-references: GDB:119794; OMIM:120210
                              Residues: 1-4,233-267 <MUR2>
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Best Loc Matches

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R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
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                                                                                                                                                                                                                                                                     Query Match 30.1%; Score 47.5; DB 2; Length 935; Best Local Similarity 48.3%; Pred. No. 1.1e+02; Matches 14; Conservative 4; Mismatches 8; Indels
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C; Accession: F85833
R; Perna, N.T.; Plun
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yegs protein - Escherichia coli (strain K-12)
Cispecias: Escherichia coli
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Riblatner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CG
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-1105 < BLAT>
A;Residues: 1-1105 < BLAT>
A;Residues: 1-1105 < BLAT>
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Genetics:
A;G

Ouery Match

30.1%; Score 47.5; DB 2; Length 1105;
Best Local Similarity 48.3%; Pred. No. 1.46+02;
Matches 14; Conservative 4; Mismatches 8; Indels 3; Gaps

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Search completed: November 10, 2004, 15:55:05 Job time : 11.9324 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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November 10, 2004, 14:50:40; Search time 53.637 Seconds (without alignments) 343.270 Million cell updates/sec OM protein - protein search, using sw model Run on:

·US-10-092-750-67 158 1 MDTIKGFDLITNFQVVADALNISLLPNPLATA 32

Title:
Perfect score: 3
Sequence: 3 Scoring table:

1825181 seqs, 575374646 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_02:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	1	Q612h0 picrophilus			ď		$\simeq$	ပ္ပ	Cae48764 corynebac	g	Aar39201 nanoarcha	O80213 methanobact					Q9yvil melanoplus		വ			Q6btd4 debaryomyce		Q71sz2 scombridae	Aaq14279 scombrida	O50152 streptomyce	Q896z2 clostridium			Q6f1t9 mesoplasma	
SUMMARIES	ID	Qecons	Q6L2H0	Q9YD78	Q6D3R8	Q6LQ81	CAG20545	085506	Q6NJY2	CAE48764	Q74NJ5	AAR39201	080213	036002	Q8KCF2	QEFCVO	Q6FA70	Q9YVI1	Oenixa .	CAE49155	Q7RH86	Q6FR20	Q6BTD4	ОЭКНЛВ	071822	AAQ14279	050152	Q896Z2	PRTB_ERWCH	Q7RMX3	Q6F1T9	Q889L4
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P20025 zea mays (m 01556 trichomonas Q27820 trichomonas Q7xyu3 qossypium h Q8y7u1 listeria mo Q720r2 listeria mo Q720r2 listeria mo Q854x1 clostridium Q9sxh2 ipomoea bat P52948 homo sapien Q7mtp3 porphyromon Q75uw4 planomonos Bad08678 planomonos Q8id93 plasmodium
MYB3 MAIZE 015556 027820 07XYU3 ACKZ LISMO 0720R2 AAT03952 AAT03952 0954M1 0954M1 0957MTP3 075VTP3 075VTP3 075VTP3 075VTP3
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## ALIGNMENTS

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STRAIN-SCRII043;
Bell K. S., Sebalina M., Pritchard L., Holden M., Hyman L.J.,
Holeva M.C., Thomson N.R., Bentley S.D., Churcher C., Mungall K.,
Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
Praser A., Hanser H., Jagels K., Moule S., Norbertczak H.,
Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
Salmond G.P.C., Birch P.R.J., Barrell B.G., Parkhill J., Toth I.K.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
ATP-binding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome analysis of Photobacterium profundum reveals the complexity of
                                                                                                                                                                                                           01-0CT-2004 (TrEWBLrel. 28, Created)
01-0CT-2004 (TrEWBLrel. 28, Last sequence update)
01-0CT-2004 (TrEWBLrel. 28, Last sequence update)
01-0CT-2004 (TrEWBLrel. 28, Last annotation update)
Putrescine transport 38, Last annotation update)
Name=potG; ORFNames=ECA2676;
Barteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriacea; Pectobacterium.
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Name=MW2219; OrderedLocusNames=PBPRA2147;

Abocobacterium profundum (Photobacterium sp. (strain SS9)).

Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Photobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32.9%; Score 52; DB 2; Length 487;
45.5%; Pred. No. 76;
tive 3; Mismatches 9; Indels
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Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR378670; CAG20545.1;
InterPro; IPR004770; Antiport_nhaC.
InterPro; IPR011014; MSCS_transeembr.
Pfam; PF03553; Na H antiporter; 1.
IIGRPAMS; TIGR00931; antiport_nhaC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              377 AA; 41989 MW; 4B24588EC144C50A CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 32.9%; Score 52; DB Local Similarity 43.5%; Pred. No. 58; es 10; Conservative 6; Mismatches
270 VEGFDVVPVDEPVVECLQLRLLGHPVARA 298
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Best Local Similarity 45.5%
Matches 10, Conservative
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                                                                                                                                                                 PRELIMINARY;
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SEQUENCE 487 AA;
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Q6LQ81;
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                                                                                              RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Puetterer O., Angelov A., Liesegang H., Gottschalk G., Schleper C., Schepers B., Dock C., Antranikian G., Liebl W., "Genome sequence of Picrophilus torridus and its implications for life around pH 0.";
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Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
Hosoyama A., Fukui S., Nagai Y., Nishijima Y., Nakazawa H.,
Takamiya M., Mauda S., Funahashi T., Tanaka T., Kudoh Y.,
Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
"Complete genome sequence of an aerobic hyper-thermophilic
DNA Res. 6.83-101(1999).
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32.9%; Score 52; DB 2; Length 321;
Best Local Similarity 34.5%; Pred. No. 49;
Matches 10; Conservative 9; Mismatches 10; Indels
                                                                                                                                                                                                                                    Archaea, Buryarchaeota, Thermoplasmata, Thermoplasmatales,
Picrophilaceae, Picrophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.5%; Score 53; DB 2; Length 309; 42.3%; Pred. No. 34; tive 3; Mismatches 12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome; Hypothetical protein.
SEGUENCE 321 AA; 35976 MW; P55FB92792299ClD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       309 AA; 34736 MW; 79E14F6540759692 CRC64;
                                                                      05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Muramoyletrapeptide carboxypeptidase (EC 3.4.17.13)
OrderedLocusNames=PT00247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UTM-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein ABE1034.
OrderedLocusNames=APE1034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 101:9091-9096 (2004).

EMBL, AE01261, AAT42832.1, -...

GO, GO:0004180; P:carboxypeptidase activity; IEA.

GO, GO:0016787; F:hydrolase activity; IEA.

InterPro; IPR003507; Peptidase U61.

Pfam; PF02016; Peptidase_U61; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 IKGFDLITNFQVVADALNISLLDNPLATA 32 :: | | | : | : | : | : | |
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                                          (TrEMBLrel. 27, Created)
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                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=DSM 9790 / ATCC 700027;
PubMed=15184674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Desulfurococaceae; Aeropyrum.
NCBI_TaxID=56636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 42.33
Matches 11; Conservative
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                                                                                                                                                                                                               Picrophilus torridus.
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SEQUENCE 309 AA
                                                                                                                                                                                                                                                                                                          NCBI_TaxID=82076;
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                                             -JUL-2004
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STRAIN=K1;
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"Analysis of the env gene of a molecularly cloned and biologically active Moloney mink cell focus-forming proviral DNA.";
"Virol. 44:19-31(1982).
EMBL; J02254; AAA46517.1; -.
HSSP; P03385; IMOF.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019028; F:structural molecule activity; IEA.
InterPro; IPR002050; Env_polyprotein.
InterPro; IPR008981; FwuLvrecept-bind.
Ffan; PF00429; TLV_coat; 1.
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Bosselman R.A., van Straaten F., van Beveren C.P., Verma I.M.,
                                                                                                                                                                                                                            Photobacterium profundum (Photobacterium sp. (strain SS9)).
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Photobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 487;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cestaro A.;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR378670; CAG20645.1; -.
SEQUENCE 487 AA; 51332 MW; D56453B148B800DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Env polyprotein.
Murine leukemia virus.
Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
NCBI_TaxID=11786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              high pressure adaptations.";
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases
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Potential.
FB242484A547CA81 CRC64;
                                                                              10-MAY-2004 (TrEMBLrel. 27, Created)
10-MAY-2004 (TrEMBLrel. 27, Last sequence update)
10-MAY-2004 (TrEMBLrel. 27, Last annotation update)
Putative Na+/H+ antiporter.
MW2219 OR PBPRA2147.
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Last annotation update)
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7
                            487 AA.
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01-NOV-1996 (TERBLEL) 01, Created)
01-NOV-1996 (TERBLEL) 01, Last seq
01-NAR-2004 (TERBLEL) 26, Last ann
                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              277 VQĞFSLQQGFQAYVDGFNISML 298
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636 AA; 69461 MW;
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SEQUENCE FROM N.A.
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MEDLINE=22965443; PubMed=14602910;
Cerdeno-Tarraga A.-M., Efstratiou A., Dover L.G., Holden M.T.G.,
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DNA polymerase III subunit gamma/tau (EC 2.7.7.7).
Name=dnaX; Synonyms=dnaZX; OrderedLocusNames=DIP0259;
Corynebacterium diphtheriae.
Corynebacteriae, Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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Bacteria, Actinobacteridae, Actinomycetales, Corynebacterineae, Corynebacterineae, Corynebacterineae, NCBI_TaxID=1717,
  Length 636;
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02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DNA polymerase III subunit gamma/tau (EC 2.7.7.7).
DNAX OR DNAZX OR DIP0259.
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41.9%; Pred. No. 1.1e+02;
ive 3; Mismatches 15;
Score 52; DB 2;
Pred. No. 1e+02;
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Query Match
Best Local Similarity 40.0
Matches 12; Conservative
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STRAIN=Kin4-M;
MEDLINE=22946215; PubMed=14566062;
Waters E., Hohn M.J., Ahel I., Graham D.E., Adams M.D., Barnstead M.,
Beson K.Y., Bibbs L., Bolanos R., Keller M., Kretz K., Lin X.,
Beson K.Y., Bibbs L., Bolanos R., Keller M., Sutton G.G., Simon M.,
Soell D., Stetter K.O., Short J.M., Noorderwier M.;
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evolution and derived parasitism.";
Proc. Natl. Acad. Sci. U.S.A. 100:12984-12988(2003).
EMBL; AE017199; AAR39201.1; -.
SEQUENCE 209 AA; 23996 MW; 660B36C348A59967 CRC64;
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MEDINE=98360012; PubMed=9694668;
Viscogliosi E., Muller M.;
"Bhylogenetic relationships of the glycolytic enzyme, glyceraldehyde-3-phosphate dehydrogenase, from parabasalid flagellates.";
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mypotherical protein.
Methanobacterium phage psiM2.
Viruses, dsDMA viruses, no RNA stage; Caudovirales; Siphoviridae.
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BMB., MFROS411, AAC27062.1; -..
PIR; T12739; T12739.
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Eukaryota, Parabasalidea, Trichomonada, Trichomonadida,
Monocercomonadidae, Monocercomonas.
NCBI_TaxID=5737;
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01-07N-1998 (TrEMBLrel. 05, Last sequence update)
01-07N-2004 (TrEMBLrel. 26, Last annotation update)
01-07N-2004 (TrEMBLrel. 26, Last annotation update)
01yeraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)
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MEDLINE=99009353; PubMed=9791169;
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SEQUENCE 26
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SEQUENCE FROM N.A.

MEDLINE=22946215; PubMed=14566062;

Maters E., Hohn M.J., Ahel I., Graham D.E., Adams M.D., Barnstead M. Beeson K.Y., Bibbs L., Bolanos R., Keller M., Kretz K., Lin X., Mathur E., Ni J., Podar M., Richardson T., Sutron G.G., Simon M., Soell D., Stetter K.O., Short J.M., Noorderwier M.;

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Nucleic Acids Res 31:6516-6523(2003).

Balb.; BAZA8354, CAR48764.1.; -.
Nucleocidyltransferaes: Transferaes.
SEQUENCE 707 AA, 75874 MW; 9AD805227F815B46 CRC64;
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32.3%; Score 51; DB 2; Length 209;
Best Local Similarity 40.0%; Pred. No. 45;
Matches 12; Conservative 6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                     32.9%; Score 52; DB 2; Length 707; 41.9%; Pred. No. 1.1e+02;
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NCBL_TaxID=160232;
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Archaea; Nanoarchaeota; Nanoarchaeum.
NCBI_TaxID=160232;
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Pfam; PF01889; DUF63; 1.
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Best Local Similarity 41.9<sup>3</sup>
Matches 13; Conservative
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SEQUENCE 209 AA
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232 TVKGFNLLTGFPDTQEISTAVLREIITTPL 261

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C STRAIN=TLS / ATCC 49552 / DSM 12025;

MEDLINE-21036885; PubMed=12093901; DOI=10.1073/pnas.132181499;

A BISEN J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,

A Dodson R.J., DeBoy R.T., Gwinn M.L., Nelson W.C., Haft D.H.,

A Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.F., Yang F.,

A Holt I.E., Umayam L.A., Mason T.M., Brenner M., Shea T.P., Caven M.B.,

A Radune D., Vamathevan J.J., Khouri H.M., White O., Gruber T.M.,

A Radune D., Vamathevan J.J., Khouri H.M., White O., Gruber T.M.,

The complete genome sequence of Chlorobium tepidum TLS, a

photosynthetic, anaerobic, green-sulfur bacterium.";

Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).

R FIGR; CT1470;
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J. Mol. Evol. 47:190-199(1998).
-!- CATALTYTC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate + NAD(+) = 3-phospho-D-glyceroy1 phosphate + NADH.
-!- PATHWAY: Second phase of glycolysis; first step.
-!- STBUITT: Honotetramer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the glyceraldehyde-3-phosphate dehydrogenase family.
EMBL; AF022420; AAC63603.1; -
HSSP: P17721; 1HDG.
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Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Rod shape-determining protein MreB.
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41.4%; Pred. No. 83;
tive 4; Mismatches
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iive 8; Mismatches
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Pfam; PF06723; MreB Mbl; I.
PRINTS; PR01652; SHAPEPROTEIN.
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Matches 11; Conservative
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ABACHER FROM N.A.

Barbe V., Vallenet D., Fonknechten N., Kreimeyer A., Oztas S.,
A Labarre L., Cruveiller S., Robert C., Duprat S., Wincker P.,
A christon L.N., Weissenbach J., Marliere P., Cohen G.N., Medique C.;
A Unique features revealed by the genome sequence of Acinetobacter sp.
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Therror; IPR001037; FAD.pyr redox.
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Therror; IPR001037; FAD.pyr redox.
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The PR00510; PR00510; PR0MDASEI.
The PR00510; PR00 Gaps 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Alxyl hydroperoxide reductase subunit F (EC 1.8.1.-).
Name-ahpF; OrderedLocusNames=ACIAD1234;
Acinecobacter sp. (strain ADF1).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Acinetobacter. 11; Length 519; Match 32.0%; Score 50.5; DB 2; Length 5 Local Similarity 32.6%; Pred. No. 1.4e+02; les 14; Conservative 7; Mismatches 11; Indels 108 INQIKGLNIKADFDVFVSLSCHNCPDVVQALNLIAIYNPNSTA 150 1 MDTIKGFDLITNFOV------VADALNISLLPNPLATA 32 Search completed: November 10, 2004, 15:53:28 PRELIMINARY;

TIKGFDLITNF---QVVADALNISLLPNPL 29

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Indels

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Sequence 9204, Ap Sequence 32069, A Sequence 19112, A popula Sequence 4678, Ap Sequence 4678, Ap Sequence 6841, Ap Sequence 5862, Ap Sequence 5862, Ap Sequence 12278, A p Sequence 12278, A p Sequence 33133, A Sequence 33133, A Sequence 31080, Ap Sequence 31133, A Sequence 31080, Ap Sequence 31133, A Sequence 31080, Ap Sequence 31080,

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US-08-276-213-3
US-09-252-9204
US-09-252-9318-3
US-08-933-7118-5
US-09-218-796A-19112
US-09-621-976-4678
US-09-621-976-4678
US-09-621-976-4679
US-09-621-976-4679
US-09-583-110-4507
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Patent No. 6590075

Patent No. 6590075

Patent No. 6590075

GENERAL INFORMATION: 0 Human Secreted Proteins FILE OF INTENTION: 07 Human Secreted Proteins FILE OF INTENTION: 07 Human Secreted Proteins FILE OF INTENTION: 07 Human Secreted Proteins FILE OF INTENTION: 07 Human Secreted Proteins FILE OF INTENTION: 07 Human Secreted Proteins FILE OF PAPLICATION NUMBER: 06/040,162

EARLIER PILING DATE: 1998-09-06

EARLIER PILING DATE: 1997-03-07

EARLIER PILING DATE: 1997-03-07

EARLIER PILING DATE: 1997-03-07

EARLIER PILING DATE: 1997-03-07

EARLIER FILING DATE: 1997-03-07

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EARLIER PILING DATE: 1997-03-07

EARLIER PILING DATE: 1997-03-07

EARLIER PILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/047, 602

EARLIER PILING DATE: 1997-05-23

EARLIER FILING DATE: 1997-05-23

EARLIER PILING DATE: 1997-05-23

EARLIER PIL
                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
   09-148-545-246
   Sequence 246, App
Sequence 5243, Ap
Sequence 5270, Ap
Sequence 7093, Ap
Sequence 5, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 9, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1136, Ap
Sequence 4517, Ap
Sequence 617, App
Sequence 863, Ap
Sequence 2, Appli
Sequence 4, Appli
Sequence 4, Appli
                                                                                                          November 10, 2004, 14:55:47; Search time 10.1779 Seconds (without alignments) 143.349 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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// /cgn2 / fptodata/1/iaa/PCTUS_COMB.pep:*
// /cgn2 / fptodata/1/iaa/PCTUS_COMB.pep:*
// /cgn2 / fptodata/1/iaa/PCTUS_COMB.pep:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-1134-0026-5243
US-09-107-5228-5270
US-09-107-5228-7093
US-09-407-427-8
US-09-407-427-8
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US-09-407-427-7
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US-09-513-990-538-2
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Maximum Match 100%
Listing first 45 summaries
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118
1 ATWMKTLQGLLDRIQAFPSSPH 22
                                                                               - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50
49.5
47
46.5
46
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44
6.5
7.4
44
44
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                                                                                                             Run on:
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No.
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	23 00/047 00/047 00/043 111 00/043 111 00/043 111 00/043	60/043,31 60/043,31 -11 60/043,67 60/043,67 60/043,67 60/048,97 60/056,88 60/056,88 60/056,88 60/056,88	ιφιφιφιφιφιφισιών
FILING DATE APPLICATION APPLICATION APPLICATION APPLICATION FILING DATE APPLICATION FILING DATE APPLICATION FILING DATE APPLICATION FILING DATE APPLICATION FILING DATE APPLICATION FILING DATE APPLICATION APPLICATION APPLICATION	APPLICATION PILLING DATE APPLICATION PILLING DATE APPLICATION PILLING DATE PILLING DATE PILLING DATE APPLICATION FILLING DATE APPLICATION PILLING DATE	APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION FILING DATE APPLICATION FILING DATE APPLICATION FILING DATE APPLICATION FILING DATE APPLICATION FILING DATE APPLICATION FILING DATE APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION	PILLING DATE: APPLICATION DATE: APPLICATION I FILLING DATE: PILLING DATE: APPLICATION I FILLING DATE: FILLING DATE: FILLING DATE: FILLING DATE: FILLING DATE: FILLING DATE: FILLING DATE: FILLING DATE: FILLING DATE:
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BARLIER FILING DATE: 1997-08-22
BARLIER APPLICATION NUMBER: 60/056,894
BARLIER APPLICATION NUMBER: 60/056,894
BARLIER APPLICATION NUMBER: 60/056,811
BARLIER APPLICATION NUMBER: 60/056,911
BARLIER APPLICATION NUMBER: 60/056,911
BARLIER APPLICATION NUMBER: 60/056,912
BARLIER FILING DATE: 1997-08-22
BARLIER APPLICATION NUMBER: 60/056,845
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BARLIER APPLICATION NUMBER: 60/047,599
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BARLIER PILING DATE: 1997-08-23
BARLIER APPLICATION NUMBER: 60/047,599
BARLIER PILING DATE: 1997-06-23
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BARLIER PILING DATE: 1997-06-23

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STATE: Massachusetts
COUNTRY: USA
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Matches 9; Conservative
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Patent No. 6583275
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES AND THERAPEUTICS
                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABPLICANT: LYND DOUGETE-Stamm et al ARINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: ENTEROCOCCUS PAECALIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US 60/0134,000C
CURRENT FILING DATE: 1999-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR PELING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                  Gaps
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0
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                                                                                                                                                                     Length 339;
                                                                                                                                                                                                                4; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THEAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                     DB 4;
                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
                                                                                                                                                                   Score 50;
Pred. No.
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COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 280
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5243, Application US/09134000C
Patent No. 6617156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Enterococcus faecalis
US-09-134-000C-5243
                                                                                                                                                                                                                                                                                                          223 TWQQALITGLLERMOTY 238
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                                                                                                                                                                Query Match
Best Local Similarity 50.0%;
Matches 8; Conservative 4
                                                                                                                                                                                                                                                             2 TWMKTLQGLLDRIQAF 17
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Matches 10; Conserv
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                                                                                            SEQ ID NO 246
LENGTH: 339
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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42.9%; Pred. No. 11;
tive 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THEABEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 30-Jun-1998
FRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
FILING DATE: 12 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
FILING DATE: July 2, 1997
ATTORNEY/AGRYT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40, 489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMULICATION: INFORMATION:
TELEPHONE: (781) 893-5007
TELEPHONE: (781) 893-5007
INFORMATION FOR SEQ ID NO: 5270:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature LOCATION: (B) L\overline{\rm O}CATION 1...369 SEQUENCE DESCRIPTION: SEQ ID NO: 5270:
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REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-01
                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINES SOURCES (Recium
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTIER: PC
OPERATING SYSTEM: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7093, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
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TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
EMATION FOR SEQ ID NO: 7093:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 TWRVTVQGISDRKTVFNPTNH 198
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SEQ ID NO 5
LENGTH: 732
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APPLICANT: ACTON, Susan L.
APPLICANT: ACTON, Keith E.
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                     5;
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COUNTRY: USA

ZOUNTRY: USA

ZOUNTRY: USA

COMPUTER: ENDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ENDABLE FORM:
COMPUTER: ENDABLE FORM:
COMPUTER: ENDABLE FORM:
CORREATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/999, 299
FILING DATE: 11-DEC-1997
CLASSIFICATION NUMBER: 35.44
ATTORNEY/AGENT INFORMATION:
NAME: ATTORNEY/AGENT INFORMATION:
TELECOMMULICATION NUMBER: 35.430
REFERENCE/DOCKET NUMBER: MA-025.01
TELECOMMULICATION NUMBER: 35.430
REFERENCE/DOCKET NUMBER: MA-025.01
TELECOMMULICATION INFORMATION:
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TELEPAX: 617-832-1000
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39.4%; Score 46.5; D
Best Local Similarity 44.0%; Pred. No. 13;
Matches 11; Conservative 1; Mismatches
                                                                                                                                                  ), NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1..362
; SEQUENCE DESCRIPTION: SEQ ID NO: 7093:
US-09-107-532A-7093
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGHAL SOURCE:
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257 TWGLLGSMPTLDSANDRLYAIPGSP 281
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Patent No. 6194556
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US-08-989-299-5
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RESULT 6 US-09-407-427-5

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| Securince 5, Application US/03407427
| Securince 5, Application US/03407427
| Securince 5, Application Oscillation US/03407427
| Securince 6, Application Oscillation Osc
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Parent No. 6610-1.

GENERAL INFORMATION:
APPLICANT: Acton, Keith E.
APPLICANT: ACTON, Keith E.
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC
TITLE OF INVENTION: ANGIOTENSIN US/09/407,427
CURRENT APPLICATION NUMBER: US/09/407,427
CURRENT PILING DATE: 1999-09-29
PRIOR PILING DATE: 1998-09-30
PRIOR PILING DATE: 1998-12-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                             GENERAL INFORMATION:
Patent No. 6194556
GENERAL INFORMATION:
APPLICANT: Acton. Susan L.
APPLICANT: Robinson, Keith B.
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
NUMBER DO SEQUENCES:
ADDRESSE: FOLEY, HOAG & ELIOT LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                       STATE:
COMPUTRY: USA
ZIP: 02109-2170
ZIP: 02109-2170
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTRE: Pachetin Release #1.0, Version #1.30
SOFTWARE: Pachetin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,299
FILING DATE: 11-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: ARTON WIMBER: 35,430
REFERENCE/DOCKET NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MIA-025.01
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Pred. No. 1e+02;
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One Post Office Square
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36.8%;
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Best Local Similarity 36.8°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
US-08-989-299-9
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ORGANISM: Rattus
  RESULT 10
US-08-989-299-9
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEEC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEEC ACID AND AMINO ACID SEQUENCES.
TITLE OF INVENTION: NUCLEEC ACID AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27544
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APPLICANT: Acton, Susan L.
APPLICANT: Acton, Susan L.
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: AND DIAGNOSTIC USES THEREFOR
TITLE OF INVENTION: AND DIAGNOSTIC USES THEREFOR
TITLE OF INVENTION: AND DIAGNOSTIC USES THEREFOR
TITLE OF INVENTION: AND DIAGNOSTIC USES THEREFOR
TITLE OF INVENTION: AND DIAGNOSTIC USES THEREFOR
CURRENT APPLICATION NUMBER: US/09/407,427
CURRENT FILING DATE: 1999-09-29
PRIOR FULING DATE: 1999-09-30
PRIOR FILING DATE: 1999-09-30
PRIOR FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 14
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  Length 1312;
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38.1%; Score 45; DB 4; Length 349;
Best Local Similarity 47.1%; Pred. No. 22;
Matches 8; Conservative 4; Mismatches 5; Indels
                                                 Indels
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  DB 3;
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Query Match 39.0%; Score 46; DB Best Local Similarity 35.0%; Pred. No. 69; Matches 7; Conservative 5; Mismatches
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Patent No. 6551795
                                                                                                                           889 WAQTWSNIYDLVAPFPSAPN 908
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                                                                                             3 WMKTLQGLLDRIQAFPSSPH 22
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Patent No. 6610497
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27544
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261 ATWSQALQAAIRQIQAY 277
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LENGTH: 1312
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EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,916
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US-09-621-976-4517
                                                                                            US-09-538-092-1136
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Sequence 1136, Application US/09538092

Patent No. 675314

Patent No. 675314

APPLICANT: Glot, Loic

APPLICANT: Glot, Loic

APPLICANT: Mansfield, Traci A.

TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542

CURRENT FILING DATE: 2000-03-28

PRIOR APPLICATION NUMBER: 60/127,352

PRIOR APPLICATION NUMBER: 60/127,352

PRIOR APPLICATION NUMBER: 60/127,352

PRIOR APPLICATION NUMBER: 60/127,352

PRIOR PILING DATE: 2000-02-01

NUMBER OF SEQ ID NOS: 1387

SOFTWARE: CURPARESEGFORMALTER Version 0.9

SEQ ID NO 1136
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; IOCATION: (239) ... (250)

OTHER INFORMATION: Description of Artificial Sequence: Full length

; CTHER INFORMATION: utrophin construct; Xaa = unknown

US-09-091-501B-10
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                                             38.1%; Score 45; DB 4; Length 1313; 36.8%; Pred. No. 1e+02;
                                                                                            8; Indels
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Tinsley, Jonathon M
APPLICANT: Davies, Kay E
TITLE OF INVENTION: Utrophin gene expression
FILE REFERENCE: 620-42
CURRENT APPLICATION NUMBER: US/09/091,5018
CURRENT APPLICATION NUMBER: US/09/091,5018
CURRENT APPLICATION NUMBER: DCT/GB96/03156
PRIOR APPLICATION NUMBER: GB 9525962.8
PRIOR FILING DATE: 1996-12-19
PRIOR FILING DATE: 1996-12-19
PRIOR FILING DATE: 1996-12-19
PRIOR FILING DATE: 1996-12-19
PRIOR FILING DATE: 1996-07-26
PRIOR PLING DATE: 1996-07-26
PRIOR PLING DATE: 1996-07-24
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
LENGTH: 3433
                                                                                            4; Mismatches
                                                                                                                                                                                                                                                       RESULT 12
US-09-031-501B-10
'S-Gquence 10, Application US/09091501B
'Patent No. 6518413
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1665 STWLYQAEALLDEIEKKPTS 1684
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                                                                                                                                                                       3 WMKTLQGLLDRIQAFPSSP 21
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                    Query Match
Best Local Similarity 36.55
Best Local 7; Conservative
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US-09-407-427-9
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                                                                                                                                                                              Query Match 38.1%; Score 45; DB 4; Length 3433; Best Local Similarity 40.0%; Pred. No. 3.1e+02; Matches 8; Conservative 5; Mismatches 7; Indels
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Sequence 4517, Application US/09621976

Parent No. 6639063

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Glordano, J.Y.

ITILE OF INVENTION: ESTS and Encoded Human Proteins.

FILE REFERENCE: GENSET. 054PR2

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT APPLICATION NUMBER: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

SEQ ID NO 4517

LENGTH: 153
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number P46939
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APPLICANT: Fischer et al.
TITLE OF INVENTION: 123 Human Secreted Proteins FILE REFERENCE: PZO10P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44.5; DE
Pred. No. 10;
6; Mismatches
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CURRENT APPLICATION NUMBER: US/08/227,357
CURRENT FILING DATE: 1999-01-08
EARLIER APPLICATION NUMBER: ECT/US98/13684
EARLIER PILING DATE: 1998-07-07
EARLIER FILING DATE: 1998-07-07
EARLIER FILING DATE: 1997-07-08
EARLIER PILING DATE: 1997-07-08
EARLIER PILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,925
EARLIER APPLICATION NUMBER: 60/051,929
EARLIER APPLICATION NUMBER: 60/051,929
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
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EARLIER FILING DATE: 1997-07-08
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EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,732
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,931
EARLIER APPLICATION NUMBER: 60/051,931
EARLIER APPLICATION NUMBER: 60/051,931
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                                                                                                                                                                                                                                                                                                      1 ATWMKTLOGLLDRIQAFPSS 20
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112 LKTL-GVLEKIQAYPEA 127
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Best Local Similarity 52.9%;
Matches 9; Conservative
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